

SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT:  
(A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
(B) STREET: 1007 MARKET STREET  
(C) CITY: WILMINGTON  
(D) STATE: DELAWARE  
(E) COUNTRY: USA  
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(I) TELEX: 6717325

(ii) TITLE OF INVENTION: PLANT AMINO ACID BIOSYNTHETIC ENZYMES

(iii) NUMBER OF SEQUENCES: 43

(iv) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: DISKETTE, 3.50 INCH  
(B) COMPUTER: IBM PC COMPATIBLE  
(C) OPERATING SYSTEM: MICROSOFT WINDOWS 95  
(D) SOFTWARE: MICROSOFT WORD VERSION 7.0A

(v) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 60/048,771  
(B) FILING DATE: JUNE 6, 1997

(vii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: MAJARIAN, WILLIAM R.  
(B) REGISTRATION NUMBER: 41,173  
(C) REFERENCE/DOCKET NUMBER: BB-1087

## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 908 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: csiln.pk0042.a3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACGGGGACA GATAAGTGGC ATGGACGAGC CGCTGGAGAT CCCTGTGCTG AACGACCTCA	60
CCATGGTTCT GGGCTCCATA GCGCAGTCGA GAGCAACCGG CGTGGTGGTC GACTTCAGCG	120
AGCCTTCAGC TGTTTACGAC AATGTCAAGC AGGCAGCGGC GTTTGGTCTG AGCAGCGTCG	180
TCTACGTTCC GAAAATCGAG CTAGAGACAG TGACTGAACT GTCAGCGTTC TGCGAGAAGG	240
CAAGCGGCTG CTTGGTTGCG CCAACGCTGT CGATTGGGTC CGTGCTCCTT CAGCAAGCGG	300
CTATACAGGC CTCGTTCCAC TACAGCAACG TTGAGATTGT GGAATCGAGA CCAAACCCAT	360
CGGATCTTCC ATCGCAAGAT GCAATCCAGA TTGCAAACAA CATATCAGAC CTTGGTCAGA	420
TATACAACAG GGAAGATATG GATTCCAGCA GTCCAGCCAG AGGCCAGCTG CTCGGGAAG	480
ACGGAGTGC GCGTGCACAGC ATGGTTCTCC CTGGTCTCGT CTCCAGCACG TCGATCAACT	540
TCTCTGGCCC AGGAGAGATG TACACCTTAC GGCATGACGT TGCGAATGTT CAGTGCCTGA	600
TGCCAGGACT GATCCTGGCG ATACGGAAGG TGGTGCGGTT CAAGAACTTG ATTTATGGC	660
TAGAGAAGTT CTTGTAGTGA ACAACAAACA ACCAATGCAA AACATCGACA GGCAACAGGC	720
AAGGCAGATA TCATCTGACG TCGCAACAAC CAAAACGACA GAGATTGGA AAATAAAGGC	780
TGCACAGAAAG ACGTCTGGGG TTTTGTGTGC ACCAGGCTGC GCAGAGAACG TCTGTCATT	840
TGTGTGCACC ACTACGGCAC TACCTGCTGA GCGCGATTTT TATAAAAAAG GCATGGGAGG	900
GAGATCAT	908

## (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 224 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: csiln.pk0042.a3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala	Gly	Gln	Ile	Ser	Gly	Met	Asp	Glu	Pro	Leu	Glu	Ile	Pro	Val	Leu
1															15

Asn Asp Leu Thr Met Val Leu Gly Ser Ile Ala Gln Ser Arg Ala Thr  
 20 25 30  
 Gly Val Val Val Asp Phe Ser Glu Pro Ser Ala Val Tyr Asp Asn Val  
 35 40 45  
 Lys Gln Ala Ala Ala Phe Gly Leu Ser Ser Val Val Tyr Val Pro Lys  
 50 55 60  
 Ile Glu Leu Glu Thr Val Thr Glu Leu Ser Ala Phe Cys Glu Lys Ala  
 65 70 75 80  
 Ser Gly Cys Leu Val Ala Pro Thr Leu Ser Ile Gly Ser Val Leu Leu  
 85 90 95  
 Gln Gln Ala Ala Ile Gln Ala Ser Phe His Tyr Ser Asn Val Glu Ile  
 100 105 110  
 Val Glu Ser Arg Pro Asn Pro Ser Asp Leu Pro Ser Gln Asp Ala Ile  
 115 120 125  
 Gln Ile Ala Asn Asn Ile Ser Asp Leu Gly Gln Ile Tyr Asn Arg Glu  
 130 135 140  
 Asp Met Asp Ser Ser Ser Pro Ala Arg Gly Gln Leu Leu Gly Glu Asp  
 145 150 155 160  
 Gly Val Arg Val His Ser Met Val Leu Pro Gly Leu Val Ser Ser Thr  
 165 170 175  
 Ser Ile Asn Phe Ser Gly Pro Gly Glu Met Tyr Thr Leu Arg His Asp  
 180 185 190  
 Val Ala Asn Val Gln Cys Leu Met Pro Gly Leu Ile Leu Ala Ile Arg  
 195 200 205  
 Lys Val Val Arg Phe Lys Asn Leu Ile Tyr Gly Leu Glu Lys Phe Leu  
 210 215 220

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: rls2.pk0017.d3

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGATTGGCA GGAGAAAATGC AGCAAAGGTC CTCTGCTCAA CGCAGATGCC GCCATCTCAG	60
AGCACAAATCA AGGTTGTTAT CATTGGGGCG ACAAAAGAGA TTGGAAGAAC GGCAATAGCG	120
GCAGTAAGTA AAGCAAGGGG AATGGAGCTT GCAGGGGCCA TAGATTCTCA GTGTATAGGC	180
CTAGATGCAG GAGAGATAAG TGGCATGGGA AGAACCCCTGG AAATTCCGGT GCTCAATGAT	240
CTCACAAATGG TTCTGGGCTC AATTGCACAA ACCAGAGCAA CTGGAGTGGT GGTTGATTT	300
AGTGAACCTT CAACTGTTA TGATAATGTC AACAGAGCA	339

## (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: rls2.pk0017.d3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys	Ile	Gly	Arg	Arg	Asn	Ala	Ala	Lys	Val	Leu	Cys	Ser	Thr	Gln	Met
1								5		10				15	

  

Pro	Pro	Ser	Gln	Ser	Thr	Ile	Lys	Val	Val	Ile	Ile	Gly	Ala	Thr	Lys
						20		25			30				

  

Glu	Ile	Gly	Arg	Thr	Ala	Ile	Ala	Ala	Val	Ser	Lys	Ala	Arg	Gly	Met
						35		40			45				

  

Glu	Leu	Ala	Gly	Ala	Ile	Asp	Ser	Gln	Cys	Ile	Gly	Leu	Asp	Ala	Gly
						50		55		60					

  

Glu	Ile	Ser	Gly	Met	Gly	Arg	Thr	Leu	Glu	Ile	Pro	Val	Leu	Asn	Asp
					65		70		75		80				

  

Leu	Thr	Met	Val	Leu	Gly	Ser	Ile	Ala	Gln	Thr	Arg	Ala	Thr	Gly	Val
							85		90		95				

  

Val	Val	Asp	Phe	Ser	Glu	Pro	Ser	Thr	Val	Tyr	Asp	Asn	Val	Lys	Gln
							100		105			110			

Ala

## (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 275 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Synechocystus sp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ala	Asn	Gln	Asp	Leu	Ile	Pro	Val	Val	Asn	Gly	Ala	Ala	Gly
1								5		10		15		

  

Lys	Met	Gly	Arg	Glu	Val	Ile	Lys	Ala	Val	Ala	Gln	Ala	Pro	Asp	Leu
					20			25			30				

  

Gln	Leu	Val	Gly	Ala	Val	Asp	His	Asn	Pro	Ser	Leu	Gln	Gly	Gln	Asp
						35		40			45				

  

Ile	Gly	Glu	Val	Val	Gly	Ile	Ala	Pro	Leu	Glu	Val	Pro	Val	Leu	Ala
						50		55		60					

Asp Leu Gln Ser Val Leu Val Leu Ala Thr Gln Glu Lys Ile Gln Gly  
 65 70 75 80

Val Met Val Asp Phe Thr His Pro Ser Gly Val Tyr Asp Asn Val Arg  
 85 90 95

Ser Ala Ile Ala Tyr Gly Val Arg Pro Val Val Gly Thr Thr Gly Leu  
 100 105 110

Ser Glu Gln Gln Ile Gln Asp Leu Gly Asp Phe Ala Glu Lys Ala Ser  
 115 120 125

Thr Gly Cys Leu Ile Ala Pro Asn Phe Ala Ile Gly Val Leu Leu Met  
 130 135 140

Gln Gln Ala Ala Val Gln Ala Cys Gln Tyr Phe Asp His Val Glu Ile  
 145 150 155 160

Ile Glu Leu His His Asn Gln Lys Ala Asp Ala Pro Ser Gly Thr Ala  
 165 170 175

Ile Lys Thr Ala Gln Met Leu Ala Glu Met Gly Lys Thr Phe Asn Pro  
 180 185 190

Pro Ala Val Glu Glu Lys Glu Thr Ile Ala Gly Ala Lys Gly Gly Leu  
 195 200 205

Gly Pro Gly Gln Ile Pro Ile His Ser Ile Arg Leu Pro Gly Leu Ile  
 210 215 220

Ala His Gln Glu Val Leu Phe Gly Ser Pro Gly Gln Leu Tyr Thr Ile  
 225 230 235 240

Arg His Asp Thr Thr Asp Arg Ala Cys Tyr Met Pro Gly Val Leu Leu  
 245 250 255

Gly Ile Arg Lys Val Val Glu Leu Lys Gly Leu Val Tyr Gly Leu Glu  
 260 265 270

Lys Leu Leu  
 275

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1012 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: chp2.pk0008.h4

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TATTGCCAGA GATGTGTGGT AATGGAGTCG GTTGCTTCGC TCGGTTTATA GCCGAGATTG	60
AAAATCTGCA GGGGACAAAT AGATTCACTA TTCTACTGG TGCTGGAAAG ATCGTTCCCTG	120
AAATACAAAG TGATGGGCAG GTAAAGGTTG ATATGGGCGA GCCTATCCTT TCTGGACTAG	180
ACATCCCCAC AAAACTGCTA GCTACCAAGA ACAAAAGCTGT TGTTCAAGCT GAATTGGCAG	240
TTGAGGGCTT AACATGGCAT GTCACATGTG TTAGCATGGG AAACCCCTCAC TGTGTCACAT	300

TTGGTGCAAA TGAGTTAAAG GTATTGCAGG TCGACGATTT AAAACTTAGC GAAATTGGC	360
CTAAATTTGA GCATCATGAA ATGTTCCCTG CTCGCACAAA CACAGAATTG GTACAGGTTT	420
TGTCTCGCTC ACACCTCAAA ATGCGGGTCT GGGAACGTGG TGCTGGAGCA ACTCTGCCT	480
GTGGTACTGG TGCTTGTGCA GTGGTTGTTG CAGCTGTTCT TGAGGGTCCA GCTGAGCGGA	540
AATGTGTAGT TGATTTGCCT GGCAGGCCAT TGGAAATTGA GTGGAGGGAG GATGACAATC	600
ATGTTTACAT GACTGGTCCT GCAGAGGTCG TCTTTATGG ATCTGTTGTT CACTAGGTAC	660
TGGGGACCAA GATAGAAGGG TTGGCTGCCA CTCAGAGCTT GTGAGATTGG TTATAGTATC	720
CATGAAACAG AGTGTCTGG TACCACTACA CTTGTTCAGA TATTCTTAAT TATGATTGCT	780
TGATTGGGT AGCMGTAGAG GCTTCCTTT GAAGCATTCT AGTGTTCMCC TTTTGACTC	840
CTTTAGTTTG TCAGGTTGA ACACATACATG GGTAACATGT CYTTCCCACC ATTTTCYGT	900
TCTTTCTTT GTAAGTGAAC GCCAATGCAG TTTTAGTATT GTTTCTATA GATTTGTCTT	960
GATGCACTGG GCTTACTACT TATTTCTGG TATGAATGCT GCCTATTTCC TG	1012

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 217 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: chp2.pk0008.h4
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Leu Pro Glu Met Cys Gly Asn Gly Val Arg Cys Phe Ala Arg Phe Ile  
 1                       5   10                                   15

Ala Glu Ile Glu Asn Leu Gln Gly Thr Asn Arg Phe Thr Ile His Thr  
 20                      25   30

Gly Ala Gly Lys Ile Val Pro Glu Ile Gln Ser Asp Gly Gln Val Lys  
 35                      40   45

Val Asp Met Gly Glu Pro Ile Leu Ser Gly Leu Asp Ile Pro Thr Lys  
 50                      55   60

Leu Leu Ala Thr Lys Asn Lys Ala Val Val Gln Ala Glu Leu Ala Val  
 65                      70   75                                   80

Glu Gly Leu Thr Trp His Val Thr Cys Val Ser Met Gly Asn Pro His  
 85                      90   95

Cys Val Thr Phe Gly Ala Asn Glu Leu Lys Val Leu Gln Val Asp Asp  
 100                     105   110

Leu Lys Leu Ser Glu Ile Gly Pro Lys Phe Glu His His Glu Met Phe  
 115                     120   125

Pro Ala Arg Thr Asn Thr Glu Phe Val Gln Val Leu Ser Arg Ser His  
 130                     135   140

Leu Lys Met Arg Val Trp Glu Arg Gly Ala Gly Ala Thr Leu Ala Cys  
 145 150 155 160  
 Gly Thr Gly Ala Cys Ala Val Val Ala Ala Val Leu Glu Gly Arg  
 165 170 175  
 Ala Glu Arg Lys Cys Val Val Asp Leu Pro Gly Gly Pro Leu Glu Ile  
 180 185 190  
 Glu Trp Arg Glu Asp Asp Asn His Val Tyr Met Thr Gly Pro Ala Glu  
 195 200 205  
 Val Val Phe Tyr Gly Ser Val Val His  
 210 215

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 481 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: rls48.pk0036.h10
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGTATCCGGC	GCCGACGGTG	TGATCTTCGT	CATGCCGGGG	GTCAATGGCG	CGGACTACAC	60
CATGAGGATC	TTCAACTCGG	ACGGCAGTGA	GCGGGAGATG	TGTGGCAATG	GAGTCCGTTG	120
CTTTGCCCGG	TTTATAGCTG	AGCTTGAAAA	CCTACAGGGA	ACACATAGCT	TCAAAATTCA	180
CACTGGCGCT	GGGCTAATCA	TTCCTGAAAT	ACAAAATGAT	GGCAAGGTAA	AGGTTGATAT	240
GGGCCAGCCC	ATTCTCTCTG	GACCAGATAT	TCCAACAAAA	CTGCCATCCA	CCAAGAATGA	300
AGCCGTTGTC	CAAGCTGATT	TGGGCAGTTG	ATGGCTAAC	ATGGCAAGTA	ACCTGTGTTA	360
GCATGGCAA	TCCACATTGT	GTCACATTG	GCACAAAGGA	GCTCAAGGTT	TTGCATGTTG	420
ATGATTAAAG	CTTAATGATA	TTGGGGCCTA	AATTCAAGCAT	CATGAAATGT	TCCTGCCCA	480
C						481

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 85 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: rls48.pk0036.h10
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Ser Gly Ala Asp Gly Val Ile Phe Val Met Pro Gly Val Asn Gly  
 1 5 10 15

Ala Asp Tyr Thr Met Arg Ile Phe Asn Ser Asp Gly Ser Glu Pro Glu  
 20 25 30

Met Cys Gly Asn Gly Val Arg Cys Phe Ala Arg Phe Ile Ala Glu Leu  
 35 40 45

Glu Asn Leu Gln Gly Thr His Ser Phe Lys Ile His Thr Gly Ala Gly  
 50 55 60

Leu Ile Ile Pro Glu Ile Gln Asn Asp Gly Lys Val Lys Val Asp Met  
 65 70 75 80

Gly Gln Pro Ile Leu  
 85

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1301 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCCCTTATT AAGCAGGGGT TTTCGCGCGC GAGACGGTGA CACTGGCAGA GTGGAATTTC	60
CGCCGCCATT CGAACGCTACA GCGATGGCCA TAACCGCCAC CATTCCGTT CCCCTCACAT	120
CCCCCAGTCG CCGCACTCTC ACCTCCGTCA ATAGCCTCTC TCCCCTTCT ACCCGATCCA	180
CTTTGCCAC ACCGCAACGC ACTTTCAAAT ACCCTAATTG GCGCCTCGTC GTGTCTTCCA	240
TGAGCACCGA AACAGCCGTC AAAACTTCAT CCGCCTCCTT CCTCAACCAG AAGGAGTCGG	300
GCTTCCTCCA TTTCGCCAAG TACCACGGCC TCGGAAACGA CTTCGTTTG ATTGACAATA	360
GAGACTCCTC CGAGCCCAAG ATCAGTGCTG AGAAAGCGGT GCAAATGTGT GATCGGAAC	420
TCGGCCTTGG AGCTGACGGA GTTATCTTG TCTTGCCTGG CATCAGTGGC ACCGATTATA	480
CCATGAGGAT TTTTAACCTCT GATGGTAGTG AGCCTGAGAT GTGTGGCAAT GGAGTTCGAT	540
GCTTGCCAA ATTTGTTCT CAGCTTGAGA ATTTACATGG GAGGCATAGT TTTACCATTC	600
ATACTGGTGC TGGTCTGATT ATTCCTGAAG TCTTGGAGGA TGGAAATGTC AGAGTTGATA	660
TGGGGGAGCC AGTTCTTAAA GCCTTGGATG TGCTACTAA ATTACCTGCA AATAAGGATA	720
ATGCTGTTGT TAAATCACAG CTAGTTGTAG ATGGAGTTAT TTGGCATGTG ACCTGTGTTA	780
GCATGGGGAA TCCACACTGT GTAACCTTCA GTAGAGAAGG AAGCCAGAA TTGCTTGTG	840
ATGAATTGAA GCTAGCAGAA ATTGGCCAA AATTGAAACA TCATGAGGTG TTCCCTGCAC	900
GAACTAACAC AGAGTTTGAG CAAAGTATTAT CTAACCTCTCA CTTGAAATG CGTGTGTTGG	960
AGCGGGGAGC AGGAGCAACC CTAGCCTGTG GAACTGGAGC TTGTGCTACT GTTGTGAG	1020
CAGTTCTTGA GGGTCGTGCT GGGAGGAATT GCACGGTTGA TCTACCTGGA GGGCCTCTTC	1080
AGATTGAGTG GAGGGAGGAA GATAATCATG TTTATATGAC AGGCTCAGCC GATGTAGTT	1140

ATTATGGTTC TTTGCCCTT TGATATGTTG CCCCCATTGT TAAACCCAAT ATGGAATTAG	1200
GAATTGGTGA ATAATATTTG TATGAGAGGT GGACTTCTG CTTGTTCCCA ATATTTGCC	1260
ACGTCTTAT AAAAAAAA AAAAAAAA AAAAAAAA A	1301

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 359 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Ile Thr Ala Thr Ile Ser Val Pro Leu Thr Ser Pro Ser Arg			
1	5	10	15
Arg Thr Leu Thr Ser Val Asn Ser Leu Ser Pro Leu Ser Thr Arg Ser			
20	25	30	
Thr Leu Pro Thr Pro Gln Arg Thr Phe Lys Tyr Pro Asn Ser Arg Leu			
35	40	45	
Val Val Ser Ser Met Ser Thr Glu Thr Ala Val Lys Thr Ser Ser Ala			
50	55	60	
Ser Phe Leu Asn Arg Lys Glu Ser Gly Phe Leu His Phe Ala Lys Tyr			
65	70	75	80
His Gly Leu Gly Asn Asp Phe Val Leu Ile Asp Asn Arg Asp Ser Ser			
85	90	95	
Glu Pro Lys Ile Ser Ala Glu Lys Ala Val Gln Leu Cys Asp Arg Asn			
100	105	110	
Phe Gly Val Gly Ala Asp Gly Val Ile Phe Val Leu Pro Gly Ile Ser			
115	120	125	
Gly Thr Asp Tyr Thr Met Arg Ile Phe Asn Ser Asp Gly Ser Glu Pro			
130	135	140	
Glu Met Cys Gly Asn Gly Val Arg Cys Phe Ala Lys Phe Val Ser Gln			
145	150	155	160
Leu Glu Asn Leu His Gly Arg His Ser Phe Thr Ile His Thr Gly Ala			
165	170	175	
Gly Leu Ile Ile Pro Glu Val Leu Glu Asp Gly Asn Val Arg Val Asp			
180	185	190	
Met Gly Glu Pro Val Leu Lys Ala Leu Asp Val Pro Thr Lys Leu Pro			
195	200	205	
Ala Asn Lys Asp Asn Ala Val Val Lys Ser Gln Leu Val Val Asp Gly			
210	215	220	
Val Ile Trp His Val Thr Cys Val Ser Met Gly Asn Pro His Cys Val			
225	230	235	240
Thr Phe Ser Arg Glu Gly Ser Gln Asn Leu Leu Val Asp Glu Leu Lys			
245	250	255	

Leu Ala Glu Ile Gly Pro Lys Phe Glu His His Glu Val Phe Pro Ala  
 260 265 270  
 Arg Thr Asn Thr Glu Phe Val Gln Val Leu Ser Asn Ser His Leu Lys  
 275 280 285  
 Met Arg Val Trp Glu Arg Gly Ala Gly Ala Thr Leu Ala Cys Gly Thr  
 290 295 300  
 Gly Ala Cys Ala Thr Val Val Ala Ala Val Leu Glu Gly Arg Ala Gly  
 305 310 315 320  
 Arg Asn Cys Thr Val Asp Leu Pro Gly Gly Pro Leu Gln Ile Glu Trp  
 325 330 335  
 Arg Glu Glu Asp Asn His Val Tyr Met Thr Gly Ser Ala Asp Val Val  
 340 345 350  
 Tyr Tyr Gly Ser Leu Pro Leu  
 355

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: wlm24.pk0030.g4

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTCCACCGCC CCCTCCTCGG GCGGTGCCT CCTCCGTCCG TTCTGTGGGA ATCCGGCCCC	60
CCGCCGCGCC GTGCCCTCGA TGGCCGTGTC CGCTCCCAAG TCGCCAGCCG CGCCCTCGTT	120
CCTCGAGCGC CGCGAGTCCG AGCGCGCGCT CCACCTCGTG AAGTACCAAG GCCTCGGCAA	180
CGACTTCATA ATGGTCGACA ACAGGGATTC GGCGTACCG AAGGTGACAC CGGAGGAGGC	240
GGCGAAGCTA TGCGACCGAA ACTTTGGTA TTGGGTGCTG ATGGCGTCAT CTTCGTCCTG	300
CCGGGGGTCA ACGGCGCGGA CTACACTATG AGGATATTCA ACTCCGATGG CAGCAACCGG	360
AATGTNTGGN ATGGATTCTGT TGCTTGCTCG CTTTATACGG AGTTGAAATC TACANGGAAA	420
CATACTCAA ACAANAGGG GGCTGGATTA ATATCCTGAA ATANANACAT GNAAGTTANG	480
TNATATGGGC ACAATCTTA TGGCANATT CANAAAATGC ATCACAAAGAT AACTTNTAAA	540
ACGATTGAAT TAGGCAANAG AANTACCGTT ATAGGAACCC ATGAANCTTG TNAAATTAAG	600
GT	602

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:  
(B) CLONE: wlm24.pk0030.g4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala Leu His Phe Val Lys Tyr Gln Gly Leu Gly Asn Asp Phe Ile Met  
1 5 10 15

Val Asp Asn Arg Asp Ser Ala Val Pro Lys Val Thr Pro Glu Glu Ala  
20 25 30

Ala Lys Leu Cys Asp Arg Asn Phe Gly Xaa Gly Ala Asp Gly Val Ile  
35 40 45

Phe Val Leu Pro Gly Val Asn Gly Ala Asp Tyr Thr Met Arg Ile Phe  
50 55 60

Asn Ser Asp Gly Ser Asn Arg Asn Val Trp Xaa Gly Phe Val Ala Cys  
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 279 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Synechocystis sp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ala Leu Ser Phe Ser Lys Tyr His Gly Leu Gly Asn Asp Phe Ile  
1 5 10 15

Leu Val Asp Asn Arg Gln Ser Thr Glu Pro Cys Leu Thr Pro Asp Gln  
20 25 30

Ala Gln Gln Leu Cys Asp Arg His Phe Gly Ile Gly Ala Asp Gly Val  
35 40 45

Ile Phe Ala Leu Pro Gly Gln Gly Thr Asp Tyr Thr Met Arg Ile  
50 55 60

Phe Asn Ser Asp Gly Ser Glu Pro Glu Met Cys Gly Asn Gly Ile Arg  
65 70 75 80

Cys Leu Ala Lys Phe Leu Ala Asp Leu Glu Gly Val Glu Glu Lys Thr  
85 90 95

Tyr Arg Ile His Thr Leu Ala Gly Val Ile Thr Pro Gln Leu Leu Ala  
100 105 110

Asp Gly Gln Val Lys Val Asp Met Gly Glu Pro Gln Leu Leu Ala Glu  
115 120 125

Leu Ile Pro Thr Thr Leu Ala Pro Ala Gly Glu Lys Val Val Asp Leu  
130 135 140

Pro Leu Ala Val Ala Gly Gln Thr Trp Ala Val Thr Cys Val Ser Met  
145 150 155 160

Gly Asn Pro His Cys Leu Thr Phe Val Asp Asp Val Asp Ser Leu Asn  
                  165                   170                   175  
 Leu Thr Glu Ile Gly Pro Leu Phe Glu His His Pro Gln Phe Ser Gln  
                  180                   185                   190  
 Arg Thr Asn Thr Glu Phe Ile Gln Val Leu Gly Ser Asp Arg Leu Lys  
                  195                   200                   205  
 Met Arg Val Trp Glu Arg Gly Ala Gly Ile Thr Leu Ala Cys Gly Thr  
                  210                   215                   220  
 Gly Ala Cys Ala Thr Val Val Ala Ala Val Leu Thr Gly Arg Gly Asp  
                  225                   230                   235                   240  
 Arg Arg Cys Thr Val Glu Leu Pro Gly Gly Asn Leu Glu Ile Glu Trp  
                  245                   250                   255  
 Ser Ala Gln Asp Asn Arg Leu Tyr Met Thr Gly Pro Ala Gln Arg Val  
                  260                   265                   270  
 Phe Ser Gly Gln Ala Glu Ile  
                  275

## (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1160 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: cc2.pk0031.c9
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTCGGCTGCG	CGTCCACGGG	AGACACCTCC	GCCGCGCTCT	CGGCCTACTG	CGCAGCCGCG	60
GGAATCCCCG	CCATCGTGT	CCTGCCAGCG	GACCGCATCT	CGCTGCAGCA	GCTCATCCAG	120
CCGATCGCCA	ACGGCGCCAC	CGTGCTCTCT	CTAGACACTG	ATTTGATGG	CTGCATGCGG	180
CTCATTGCG	AGGTCACTGC	AGAGCTGCCA	ATCTACCTTG	CCAATTGCT	CAACCCGCTC	240
CGCCTTGAGG	GGCAGAAAGAC	AGCGGCCATC	GAGATATTGC	AGCAGTTCAA	TTGGCAGGTG	300
CCAGATTGGG	TCATTGTTCC	AGGAGGAAT	CTTGGGAATA	TCTATGCATT	CTACAAGGGG	360
TTTGAGATGT	GCCGCGTTCT	TGGACTTGT	GATCGCGTGC	CACGGCTTGT	CTGCGCACAG	420
GCTGCAAATG	CAAATCCATT	GTACCGGTAC	TACAAGTCAG	GTTGGACTGA	GTTTGAGCCA	480
CAAACGTCCG	AGACTACATT	TGCATCTGCG	ATACAGATTG	GTGATCCTGT	ATCTGTTGAC	540
CGTGGGGTGG	TCGCGCTGAA	GGCCACTGAC	GGTATTGTGG	AGGAGGCTAC	AGAGGAGGAG	600
CTAATGGATG	CAACGGCGCT	TGCTGACCGC	ACTGGGATGT	TTGCTTGCCC	ACATACTGGG	660
GTTGCACTTG	CTGCTTGTT	TAAGCTTCAG	GGTCAGCGTA	TAATTGGCCC	TAATGACCGC	720
ACTGTGGTTG	TTAGCACAGC	TCATGGGCTG	AAGTTCACGC	AGTCAGAGAT	TGACTACCAC	780

GACAAAAACA TCAAAGACAT GGTTGCCAG TATGCTAAC	CACCGATCAG TGTGAAGGCT	840
GACTTGGTT CTGTGATGGA TGTTCTCCAG AAAAATCTCA	ATGGTAAGAT ATAAAGTTAT	900
ATGATTAATT AACCCCTCCAA ACTGTTTTT TTTGTTTTT CGTTCCAGGA	ATTTTATTCC	960
TGAGCTTTTC AACTTGTGTT GGTGAACATG GTATGGTGCT	AAAATCTAGA CCTAATACCT	1020
TGTAGTACTA GTTCTGGAGG CTCTTTGGT TGTAGGTCGA	AGTGGATAGA GCTGTTCC	1080
GTACTTTATC TGTTTCATGT AATATGAATA ATAAATTATG	GTCTAAATAT TTGAATAAAA	1140
AATCGTTGG AATGACCCAC		1160

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 297 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: cc2.pk0031.c9

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Val Gly Cys Ala Ser Thr Gly Asp Thr Ser Ala Ala	Leu Ser Ala Tyr		
1	5	10	15
Cys Ala Ala Ala Gly Ile Pro Ala Ile Val Phe Leu	Pro Ala Asp Arg		
20	25	30	
Ile Ser Leu Gln Gln Leu Ile Gln Pro Ile Ala Asn	Gly Ala Thr Val		
35	40	45	
Leu Ser Leu Asp Thr Asp Phe Asp Gly Cys Met Arg	Leu Ile Arg Glu		
50	55	60	
Val Thr Ala Glu Leu Pro Ile Tyr Leu Ala Asn Ser	Leu Asn Pro Leu		
65	70	75	80
Arg Leu Glu Gly Gln Lys Thr Ala Ala Ile Glu Ile	Leu Gln Phe		
85	90	95	
Asn Trp Gln Val Pro Asp Trp Val Ile Val Pro Gly	Gly Asn Leu Gly		
100	105	110	
Asn Ile Tyr Ala Phe Tyr Lys Gly Phe Glu Met Cys	Arg Val Leu Gly		
115	120	125	
Leu Val Asp Arg Val Pro Arg Leu Val Cys Ala Gln	Ala Ala Asn Ala		
130	135	140	
Asn Pro Leu Tyr Arg Tyr Lys Ser Gly Trp Thr Glu	Phe Glu Pro		
145	150	155	160
Gln Thr Ala Glu Thr Thr Phe Ala Ser Ala Ile Gln	Ile Gly Asp Pro		
165	170	175	
Val Ser Val Asp Arg Ala Val Val Ala Leu Lys Ala	Thr Asp Gly Ile		
180	185	190	

Val Glu Glu Ala Thr Glu Glu Glu Leu Met Asp Ala Thr Ala Leu Ala  
 195 200 205  
 Asp Arg Thr Gly Met Phe Ala Cys Pro His Thr Gly Val Ala Leu Ala  
 210 215 220  
 Ala Leu Phe Lys Leu Gln Gly Gln Arg Ile Ile Gly Pro Asn Asp Arg  
 225 230 235 240  
 Thr Val Val Val Ser Thr Ala His Gly Leu Lys Phe Thr Gln Ser Lys  
 245 250 255  
 Ile Asp Tyr His Asp Lys Asn Ile Lys Asp Met Val Cys Gln Tyr Ala  
 260 265 270  
 Asn Pro Pro Ile Ser Val Lys Ala Asp Phe Gly Ser Val Met Asp Val  
 275 280 285  
 Leu Gln Lys Asn Leu Asn Gly Lys Ile  
 290 295

## (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 325 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: cs1.pk0058.g5
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGGCTTGCA AGTACTCCAA CCCGCCTGTG AGCGTGAAGG CTGACTTTGG CGCCGTGATG	60
GATGTGCTGA AGAAGAGGCT CAAGGGCAAG CTCTGAGCGC CTGTGCCTGG CTAATGCAAT	120
CAACTGATTG GAATGCAGTG GTTTCGTCGG TATCGGGGGG TCTTTAGGC TTCAGAAAATT	180
CTGTCGGGT TAGACTATTG GTTTGTGGAG TTTAGCAGGA GAATGGCTAT CTCTCCTGCA	240
AGACTGGCGC TCTTCCTTGT GCTACGAATG TGTTACCATG GATAATAAGT GTAGTCGCTG	300
TCGGATTGAA TAATCAAAAA AAAAN	325

## (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: cs1,pk0058.g5
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Cys Lys Tyr Ser Asn Pro Pro Val Ser Val Lys Ala Asp Phe	
1 5 10 15	

Gly Ala Val Met Asp Val Leu Lys Lys Arg Leu Lys Gly Lys Leu  
 20 25 30

## (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 528 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: rls72.pk0018.e7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACACCCAACA CGCAGACTTG ACAGATTCTG CTACTACAAA TCCTGCATAT TTAACAGCGC	60
TGCAACTCGA CGATGGAGAA CGGTGCTGCA ACCAACGGGG CGTCGGAGAA GTCGCACTCT	120
CCTTCACAGA CCTACCTCTC CACAAGGGGA GACGATTATG GGCTCTCATT CGAGACCGTC	180
GTCCTCAAAG GTCTTGCAGC TGACGGGGT CTTTCCTGC CCGAGGAAGT GCCCGCGGCA	240
ACCGAGTGGC AAAGCTGGAA AGACCTGCC TACACCGAGC TTGCCGTCAA GGTTCTCAGC	300
TTGTACATCT CCCCCGCCGA GGTGCCGACG GAAGACCTCA GGGCGCTCGT CGAGCGCAGC	360
TACTCGACCT TCCGATCCAA GGAGGTTGTG CCGCTGGTGA AGCTGGAGGA CAACCTTCAC	420
CTGCTGGAGC TATTCCACGG CCCCAACTAC TCGTTCAAGG ACTGCGCGCT GCAATTCCCT	480
GGTAACCTCN TCGAGTACTT TTGACTCNCA AGAACAAAGGG AAAGGAGG	528

## (2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 143 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: rls72.pk0018.e7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Glu Asn Gly Ala Ala Thr Asn Gly Ala Ser Glu Lys Ser His Ser  
 1 5 10 15

Pro Ser Gln Thr Tyr Leu Ser Thr Arg Gly Asp Asp Tyr Gly Leu Ser  
 20 25 30

Phe Glu Thr Val Val Leu Lys Gly Leu Ala Ala Asp Gly Gly Leu Phe  
 35 40 45

Leu Pro Glu Glu Val Pro Ala Ala Thr Glu Trp Gln Ser Trp Lys Asp  
 50 55 60

Leu Pro Tyr Thr Glu Leu Ala Val Lys Val Leu Ser Leu Tyr Ile Ser  
 65 70 75 80

Pro	Ala	Glu	Val	Pro	Thr	Glu	Asp	Leu	Arg	Ala	Leu	Val	Glu	Arg	Ser
				85					90					95	
Tyr	Ser	Thr	Phe	Arg	Ser	Lys	Glu	Val	Val	Pro	Leu	Val	Lys	Leu	Glu
			100					105					110		
Asp	Asn	Leu	His	Leu	Leu	Glu	Leu	Phe	His	Gly	Pro	Asn	Tyr	Ser	Phe
						115			120				125		
Lys	Asp	Cys	Ala	Leu	Gln	Phe	Leu	Gly	Asn	Leu	Xaa	Glu	Tyr	Phe	
						130		135				140			

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 571 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: sel.06a03
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGATGCAATG GTGCAGGCTG ATTCCACTGG AATGTTCAT A TGTCCACACA CTGGGGTGGC 60  
TCTGGCGGCG CTTATTAAGC TGAGGAATCG TGGGGTTATC GGTGCCGGTG AGAGGGTTGT 120  
GGTGGTGAGC ACTGCACATG GATTGAAGTT TGCACAGAGC AAGATTGATT ATCATTCTGG 180  
GCTCATTCCCT GGAATGGGCC GCTATGCTAA CCCGCTGGTT TCGGTTAAGG CGGATTTGG 240  
ATCGGTCTATG GATGTTCTCA AGGATTCTTG CACAACAAGT CCCCCGACTT TAACAAGTCT 300  
TGACGTTGCC AAGTAAGTT TAGTCGGGG TTTTTCTGA TAAAGATGT TTTTAAACAT 360  
GTTTGTGTNC ACTTCGGTC GTTATTATGG ATTTGTAAGA TTGGGCCAA GTATCGAGG 420  
GTTTGATTTC AAACAACATG CTTCTGGTGA CGCAATGCAA ATTCGGNGC ATAACATCAT 480  
TGTGAAAGAT GGATCNCGAC CGATGAAACT GTGTGGCAAG TAATGAGAAG AAAATAGGGC 540  
ACTTGTACAG AGATTTNAAA GNTTAATTTC N 571

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 104 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: sel.06a03
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Asp Ala Met Val Gln Ala Asp Ser Thr Gly Met Phe Ile Cys Pro His  
 1 5 10 15

Thr Gly Val Ala Leu Ala Ala Leu Ile Lys Leu Arg Asn Arg Gly Val  
 20 25 30  
 Ile Gly Ala Gly Glu Arg Val Val Val Val Ser Thr Ala His Gly Leu  
 35 40 45  
 Lys Phe Ala Gln Ser Lys Ile Asp Tyr His Ser Gly Leu Ile Pro Gly  
 50 55 60  
 Met Gly Arg Tyr Ala Asn Pro Leu Val Ser Val Lys Ala Asp Phe Gly  
 65 70 75 80  
 Ser Val Met Asp Val Leu Lys Asp Ser Cys Thr Thr Ser Pro Pro Thr  
 85 90 95  
 Leu Thr Ser Leu Asp Val Ala Lys  
 100

## (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2191 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: srl.pk0003.f6

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCTTCCTCTT	CTCTGTTCA	GTCTCTCCCT	TTCTCTCTCC	AAACCTCTAA	ACCCTACGCG	60
CCTCCCAAAC	CCGCCGCCCA	CTTCGTTGTC	CGCGCCCAAT	CCCCCCTCAC	TCAGAACAAAC	120
AACTCCTCCT	CCAAGCATCG	CCGCCCCGCC	GACGAGAACAA	TCCGCGACGA	GGCCCGCCGC	180
ATCAATGCGC	CCCACGACCA	CCACCTCTTC	TCGGCCAAGT	ACGTCCCCTT	CAACGCCGAC	240
TCCTCCTCCT	CCTCCTCCAC	GGAGTCCTAC	TCGCTCGACG	AGATCGTCTA	CCGCTCCCAA	300
TCCGGCGGCC	TCCTGGACGT	CCAGCACGAC	ATGGATGCC	TCAAGCGTTT	CGACGGCGAG	360
TACTGGCGCA	ACCTCTTCGA	CTCGCGCGTG	GGCAAAACCA	CCTGGCCTTA	CGGCTCCGGC	420
GTCTGGAGCA	AAAAAGAATG	GGTCCTCCCC	GAGATCCACG	ACGACGATAT	CGTCTCCGCC	480
TTCGAGGGTA	ACTCCAACCT	CTTCTGGGCC	GAGCGTTTCG	GCAAACAGTT	CCTCGGCATG	540
AACGATTGTG	GGGTCAAACA	CTGCGGAATC	AGCCACACGG	GCAGCTCAA	GGATCTCGGC	600
ATGACCGTCC	TCGTCAGCCA	GGTCAATCGC	TTGAGAAAAA	TGAACCGCCC	CGTCGTCGGT	660
GTTGGTTGCG	CCTCCACCGG	TGACACATCG	GCCGCTTTAT	CCGCCTATTG	CGCTTCCGCT	720
GCCATTCCCT	CCATTGTGTT	TTTGCCTGCT	AATAAAATCT	CTCTTGCCCA	ACTTGTTCAG	780
CCTATTGCCA	ATGGAGCCTT	TGTGTTGAGT	ATCGACACTG	ATTTGATGG	TTGCATGCAG	840
TTGATCAGAG	AAGTCACTGC	TGAATTGCCT	ATTATTTGG	CTAACTCTCT	CAACAGTTG	900
AAGTTGGAAG	GGCAGAAAAC	TGCTGCTATT	GAGATTCTGC	AGCAGTTGA	TTGGCAGGTT	960
CCTGATTGGG	TCATTGTGCC	TGGAAGCAAC	CTTGGCAACA	TTTATGCCCT	TTACAAAGGG	1020

TTTAAGATGT TTCAAGAGCT TGGGCTTGTG GATAAGATT CAAAGGCTTGT TTGTGCTCAG	1080
GCTGCCAATG CTGATCCTTT GTATTTGTAC TTTAAATCCG GGTGGAAGGA GTTTAAGCCT	1140
GTGAAGTCGA GCACTACATT TGCTTCTGCC ATTCAAATTG GTGATCCTGT TTCCATTGAC	1200
AGGGCGGTTTC ACGCGCTAAA GAGTTGCGAT GGGATTGTGG AGGAGGCCAC GGAGGAGGAG	1260
TTGATGGATG CTACAGCGCA GGCAGGATTCT ACTGGGATGT TTATTTGCC CCACACCAGG	1320
GTTGCTTTAA CTGCATTGTT TAAGCTCAGG AACAGCGGGG TTATTAAGGC CACTGATAGG	1380
ACTGTGGTGG TTAGCACTGC TCATGGCTTG AAGTTCACTC AGTCCAAGAT TGATTACCAT	1440
TCTAAGGACA TCAAGGACAT GGCTTGCAGC TATGCTAACCG CGCCCATGCA AGTGAAGGCA	1500
GACTTTGGCT CGGTTATGGA TGTTTGAAG ACGTATTTGC AGAGTAAGGC TCATTAGGTT	1560
AGCATTGCAA GTTTGCTCC TCCTGAGTTT GCTCATTATT TACTTACTTT TAGGCACTAC	1620
TGCTGTATTG TCTTTCTAT GAGCTAGGTT TGAGTGTGTT AATAATTGC TTGCTGCATT	1680
ATGTATGCCG TCTAGTGTTC CATATTGGC ATCATCCTTA GTATTTGTG TAGATTTCT	1740
TTGCTGAGCA TTGATATAA TAGCTCAAGT AGGAAAATGA ATTGGGTACT ATGAGGAATG	1800
CATATCATTG GCTTGTTATT ACTGGATTCC AGACCACCCC AAAAGAAAAT AATTCCAAAA	1860
AATATAATTAA GAACAAATTG CGTCCTGTT ATGCTGTTGG CATTAAAGCTC AGTGTGGTGA	1920
TTACCAAGCA ACTCGAAATC AAGAGAAAAA AAAATTGACA GCAAAGGAGC TGCATTGTTG	1980
GACTGAGTCA CATCACTTCA TTGCTATGTC GTCATATTTC GTTGAATTAC GGGAAAGGCAG	2040
CATGCACAGC AATATGCAGC GATTAACGTAGA AGCCACACCG CACACATTGA AGTAGTAGTC	2100
AATTTAGACA CTCCATCTTG TACTTCTAC AAAATGAAT TTTCTTAGC CATTAAAGTAT	2160
AATATTTTAT TCTAAAAAAA AAAAAAAAAA A	2191

## (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 518 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: sr1.pk0003.f6

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ala Ser Ser Ser Leu Phe Gln Ser Leu Pro Phe Ser Leu Gln Thr Ser			
1	5	10	15

Lys Pro Tyr Ala Pro Pro Lys Pro Ala Ala His Phe Val Val Arg Ala		
20	25	30

Gln Ser Pro Leu Thr Gln Asn Asn Asn Ser Ser Lys His Arg Arg		
35	40	45

Pro Ala Asp Glu Asn Ile Arg Asp Glu Ala Arg Arg Ile Asn Ala Pro  
 50 55 60  
 His Asp His His Leu Phe Ser Ala Lys Tyr Val Pro Phe Asn Ala Asp  
 65 70 75 80  
 Ser Ser Ser Ser Ser Thr Glu Ser Tyr Ser Leu Asp Glu Ile Val  
 85 90 95  
 Tyr Arg Ser Gln Ser Gly Gly Leu Leu Asp Val Gln His Asp Met Asp  
 100 105 110  
 Ala Leu Lys Arg Phe Asp Gly Glu Tyr Trp Arg Asn Leu Phe Asp Ser  
 115 120 125  
 Arg Val Gly Lys Thr Thr Trp Pro Tyr Gly Ser Gly Val Trp Ser Lys  
 130 135 140  
 Lys Glu Trp Val Leu Pro Glu Ile His Asp Asp Asp Ile Val Ser Ala  
 145 150 155 160  
 Phe Glu Gly Asn Ser Asn Leu Phe Trp Ala Glu Arg Phe Gly Lys Gln  
 165 170 175  
 Phe Leu Gly Met Asn Asp Leu Trp Val Lys His Cys Gly Ile Ser His  
 180 185 190  
 Thr Gly Ser Phe Lys Asp Leu Gly Met Thr Val Leu Val Ser Gln Val  
 195 200 205  
 Asn Arg Leu Arg Lys Met Asn Arg Pro Val Val Gly Val Gly Cys Ala  
 210 215 220  
 Ser Thr Gly Asp Thr Ser Ala Ala Leu Ser Ala Tyr Cys Ala Ser Ala  
 225 230 235 240  
 Ala Ile Pro Ser Ile Val Phe Leu Pro Ala Asn Lys Ile Ser Leu Ala  
 245 250 255  
 Gln Leu Val Gln Pro Ile Ala Asn Gly Ala Phe Val Leu Ser Ile Asp  
 260 265 270  
 Thr Asp Phe Asp Gly Cys Met Gln Leu Ile Arg Glu Val Thr Ala Glu  
 275 280 285  
 Leu Pro Ile Tyr Leu Ala Asn Ser Leu Asn Ser Leu Lys Leu Glu Gly  
 290 295 300  
 Gln Lys Thr Ala Ala Ile Glu Ile Leu Gln Gln Phe Asp Trp Gln Val  
 305 310 315 320  
 Pro Asp Trp Val Ile Val Pro Gly Ser Asn Leu Gly Asn Ile Tyr Ala  
 325 330 335  
 Phe Tyr Lys Gly Phe Lys Met Phe Gln Glu Leu Gly Leu Val Asp Lys  
 340 345 350  
 Ile Pro Arg Leu Val Cys Ala Gln Ala Ala Asn Ala Asp Pro Leu Tyr  
 355 360 365  
 Leu Tyr Phe Lys Ser Gly Trp Lys Glu Phe Lys Pro Val Lys Ser Ser  
 370 375 380  
 Thr Thr Phe Ala Ser Ala Ile Gln Ile Gly Asp Pro Val Ser Ile Asp  
 385 390 395 400

Arg Ala Val His Ala Leu Lys Ser Cys Asp Gly Ile Val Glu Glu Ala  
 405 410 415  
 Thr Glu Glu Glu Leu Met Asp Ala Thr Ala Gln Ala Asp Ser Thr Gly  
 420 425 430  
 Met Phe Ile Cys Pro His Thr Gly Val Ala Leu Thr Ala Leu Phe Lys  
 435 440 445  
 Leu Arg Asn Ser Gly Val Ile Lys Ala Thr Asp Arg Thr Val Val Val  
 450 455 460  
 Ser Thr Ala His Gly Leu Lys Phe Thr Gln Ser Lys Ile Asp Tyr His  
 465 470 475 480  
 Ser Lys Asp Ile Lys Asp Met Ala Cys Arg Tyr Ala Asn Pro Pro Met  
 485 490 495  
 Gln Val Lys Ala Asp Phe Gly Ser Val Met Asp Val Leu Lys Thr Tyr  
 500 505 510  
 Leu Gln Ser Lys Ala His  
 515

## (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 643 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: wr1.pk0085.h2
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCTCATCCAG CCCATGCCA ACGGCGCCAC GGTGCTCTCG CTTGACACGG ATTCGACGG	60
ATGCATGCGG CTTATCAGGG AGGTGACAGC TGAGCTGCCA ATATACCTCG CAAACTCACT	120
CAAECTCGCTT CCGGCTGGAG GGGCAGAAGA CTGCAGCCAT CCGAGATATT GCAACANTCA	180
ATTGGCAGGT GCCCGGACTG GGTACACATCC CAAGGAGGCA ATCTGGGGGA ACATTTATG	240
CTTTCTACA AGGATTTNAA TTTCCGTGTC CTTNGCTAGT TGATTNCCTT CCNACTCCTT	300
GTTANTNCAA NAGGCCGCCA ACGCAAACCC ACTGTACCCG TACTACAATC CTGGGGTGAC	360
TGATTTCCAT CCACTTGNTT GCCGGGACAA TTTNCATCCN GCAACAATTT GGGGATTCCA	420
TATCNATTAC CNTCGGTTTT TTCNCCTNA AAGGACNNAT GATTNTCCNA GGAACTCCNN	480
AGGNNGGATCA AGGATCCAAA GGCTTCTAC TCACTGGAAN TTGCTTCCA ANACGGGTT	540
CACTNCCGCC CGTTAAACCC NTGACAAGTA TAATGGACAA CACNCCGGGG TNTATNACAA	600
CGGCAANTTN AAANCAAGTT NATCATTAGA ACNGGAANTT NCC	643

## (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 84 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: wr1.pk0085.h2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Leu Ile Gln Pro Ile Ala Asn Gly Ala Thr Val Leu Ser Leu Asp Thr  
 1 5 10 15

Asp Phe Asp Gly Cys Met Arg Leu Ile Arg Glu Val Thr Ala Glu Leu  
 20 25 30

Pro Ile Tyr Leu Ala Asn Ser Leu Asn Ser Leu Xaa Leu Glu Gly Gln  
 35 40 45

Lys Thr Ala Ala Ile Arg Asp Ile Ala Thr Xaa Asn Trp Gln Val Pro  
 50 55 60

Gly Leu Gly His Ile Pro Arg Arg Gln Ser Xaa Thr Phe Tyr Ala Phe  
 65 70 75 80

Leu Gln Gly Phe

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 525 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Arabidopsis thaliana

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Leu Ser Ser Cys Leu Phe Asn Ala Ser Val Ser Ser Leu Asn Pro Lys  
 1 5 10 15

Gln Asp Pro Ile Arg Arg His Arg Ser Thr Ser Leu Leu Arg His Arg  
 20 25 30

Pro Val Val Ile Ser Cys Thr Ala Asp Gly Asn Asn Ile Lys Ala Pro  
 35 40 45

Ile Glu Thr Ala Val Lys Pro Pro His Arg Thr Glu Asp Asn Ile Arg  
 50 55 60

Asp Glu Ala Arg Arg Asn Arg Ser Asn Ala Val Asn Pro Phe Ser Ala  
 65 70 75 80

Lys Tyr Val Pro Phe Asn Ala Ala Pro Gly Ser Thr Glu Ser Tyr Ser  
 85 90 95

Leu Asp Glu Ile Val Tyr Arg Ser Arg Ser Gly Gly Leu Leu Asp Val  
 100 105 110

Glu His Asp Met Glu Ala Leu Lys Arg Phe Asp Gly Ala Tyr Trp Arg  
 115 120 125

Asp Leu Phe Asp Ser Arg Val Gly Lys Ser Thr Trp Pro Tyr Gly Ser  
 130 135 140  
 Gly Val Trp Ser Lys Lys Glu Trp Val Leu Pro Glu Ile Asp Asp Asp  
 145 150 155 160  
 Asp Ile Val Ser Ala Phe Glu Gly Asn Ser Asn Leu Phe Trp Ala Glu  
 165 170 175  
 Arg Phe Gly Lys Gln Phe Leu Gly Met Asn Asp Leu Trp Val Lys His  
 180 185 190  
 Cys Gly Ile Ser His Thr Gly Ser Phe Lys Asp Leu Gly Met Thr Val  
 195 200 205  
 Leu Val Ser Gln Val Asn Arg Leu Arg Lys Met Lys Arg Pro Val Val  
 210 215 220  
 Gly Val Gly Cys Ala Ser Thr Gly Asp Thr Ser Ala Ala Leu Ser Ala  
 225 230 235 240  
 Tyr Cys Ala Ser Ala Gly Ile Pro Ser Ile Val Phe Leu Pro Ala Asn  
 245 250 255  
 Lys Ile Ser Met Ala Gln Leu Val Gln Pro Ile Ala Asn Gly Ala Phe  
 260 265 270  
 Val Leu Ser Ile Asp Thr Asp Phe Asp Gly Cys Met Lys Leu Ile Arg  
 275 280 285  
 Glu Ile Thr Ala Glu Leu Pro Ile Tyr Leu Ala Asn Ser Leu Asn Ser  
 290 295 300  
 Leu Arg Leu Glu Gly Gln Lys Thr Ala Ala Ile Glu Ile Leu Gln Gln  
 305 310 315 320  
 Phe Asp Trp Gln Val Pro Asp Trp Val Ile Val Pro Gly Gly Asn Leu  
 325 330 335  
 Gly Asn Ile Tyr Ala Phe Tyr Lys Gly Phe Lys Met Cys Gln Glu Leu  
 340 345 350  
 Gly Leu Val Asp Arg Ile Pro Arg Met Val Cys Ala Gln Ala Ala Asn  
 355 360 365  
 Ala Asn Pro Leu Tyr Leu His Tyr Lys Ser Gly Trp Lys Asp Phe Lys  
 370 375 380  
 Pro Met Thr Ala Ser Thr Thr Phe Ala Ser Ala Ile Gln Ile Gly Asp  
 385 390 395 400  
 Pro Val Ser Ile Asp Arg Ala Val Tyr Ala Leu Lys Lys Cys Asn Gly  
 405 410 415  
 Ile Val Glu Glu Ala Thr Glu Glu Leu Met Asp Ala Met Ala Gln  
 420 425 430  
 Ala Asp Ser Thr Gly Met Phe Ile Cys Pro His Thr Gly Val Ala Leu  
 435 440 445  
 Thr Ala Leu Phe Lys Leu Arg Asn Gln Gly Val Ile Ala Pro Thr Asp  
 450 455 460  
 Arg Thr Val Val Val Ser Thr Ala His Gly Leu Lys Phe Thr Gln Ser  
 465 470 475 480

Lys Ile Asp Tyr His Ser Asn Ala Ile Pro Asp Met Ala Cys Arg Phe  
485 490 495

Ser Asn Pro Pro Val Asp Val Lys Ala Asp Phe Gly Ala Val Met Asp  
500 505 510

Val Leu Lys Ser Tyr Leu Gly Ser Asn Thr Leu Thr Ser  
515 520 525

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1478 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: cen1.pk0064.f4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAACAGTGGT CCTTGAGGGG GACTCATATG ATGAAGCTCA GTCATATGCA AAATTGCGTT	60
GCCAGCAGGA AGGCCGCACA TTTGTACCTC CTTTGACCA TCCTGATGTC ATCACTGGAC	120
AAGGAACATAT CGGCATGGAA ATTGTTAGGC AGCTGCAAGG TCCACTGCAT GCAATATTTG	180
TACCTGTTGG AGGTGGTGGG TTAATTGCTG GAATTGCTGC CTATGTAAAA CGGGTTCGCC	240
CAGAGGTGAA AATAATTGGA GTGGAACCC CAGATGCAAA TGCAATGGCA TTATCCTTGT	300
GTCATGGTAA GAGGGTCATG TTGGAGCATG TTGGTGGGTT TGCTGATGGT GTAGCTGTCA	360
AAGCTGTTGG GGAAGAACCA TTTCGCTGT GCAGAGAGCT AGTAGATGGC ATTGTTATGG	420
TCAGTCGAGA TGCTATTGTT GCTTCAATAA AGGATATGTT TGAGGAGAAA AGAAGTATCC	480
TTGAACCTGC TGGTGCCCTT GCATTGGCTG GGGCTGAAGC CTACTGCAAA TACTATAACT	540
TGAAAGGAGA AACTGTGGTT GCAATAACTA GTGGGGCAAA TATGAACCTT GATCGACTTA	600
GACTAGTAAC CGAGCTAGCT GATGTTGCC GAAAACGGGA AGCACTGTTA GCTACATTG	660
TGCCAGAGCG GCAGGGAAAGC TTCAAAAAAT TCACAGAATT GGTTGGCAGG ATGAATATTA	720
CTGAATTCAA ATACAGATAC GATTCTAATG CAAAGATGC CCTTGTCTT TACAGTGGT	780
GCATCTACAC TGACAATGAG CTTGGAGCAA TGATGGATCG CATGGAATCT GCGAAACTGA	840
GGACTGTTAA CCTTACTGAC AATGATTGG CAAAGGACCA CCTTAGATAC TTTATTGGAG	900
GAAGATCAGA AATAAAAGAT GAACTGGTT ACCGGTTCAT TTTCCCGGAA AGGCCTGGGG	960
CCCTTATGAA ATTTTGAC ACGTTAGTC CTCGTTGGAA CATCAGCCTT TTCCATTACC	1020
GTGCACAGGG TGAAGCTGGA GCAAATGTAT TAGTTGGTAT ACAAGTGCCG CCAGCAGAAT	1080
TTGATGAATT CAAGAGTCAT GCCAACAAATC TTGGGTACGA GTACATGTCA GAGCACAAACA	1140
ATGAGATATA CCGGTTGCTG TTGCGTGACC CAAAGGTCTA ATGTATATGC CTTTGCTCCC	1200
ATAATAAGTT GGTGACACTT TTCAAGGAAG ATTTGCTCC AAGGTAGAAG TTGCGAGTTT	1260

CTTCAAGTTG AAATGAAGCC ATCACCAAAT GTAGCTTCGG TGTGCCATCT GTTTACTCAG	1320
TTAGATCATG TAGTGTATCA GTTGTGTATC TTTGTTGTTG TGCTTCGTGA TCTCAATTAA	1380
TTGCTTGAC CACCTAGAGG TTGTCAAATA ATGATAACCG ATATGTTATC TAAATATCTA	1440
ATAATGATTA TGTGATTGTG ATTAAAAAGG GGGGGCCC	1478

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 392 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: cen1.pk0064.f4

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Thr Val Val Leu Glu Gly Asp Ser Tyr Asp Glu Ala Gln Ser Tyr Ala  
 1                   5                   10                   15  
  
 Lys Leu Arg Cys Gln Gln Glu Gly Arg Thr Phe Val Pro Pro Phe Asp  
 20                 25                   30  
  
 His Pro Asp Val Ile Thr Gly Gln Gly Thr Ile Gly Met Glu Ile Val  
 35                 40                   45  
  
 Arg Gln Leu Gln Gly Pro Leu His Ala Ile Phe Val Pro Val Gly Gly  
 50                 55                   60  
  
 Gly Gly Leu Ile Ala Gly Ile Ala Ala Tyr Val Lys Arg Val Arg Pro  
 65                 70                   75                   80  
  
 Glu Val Lys Ile Ile Gly Val Glu Pro Ser Asp Ala Asn Ala Met Ala  
 85                 90                   95  
  
 Leu Ser Leu Cys His Gly Lys Arg Val Met Leu Glu His Val Gly Gly  
 100               105                   110  
  
 Phe Ala Asp Gly Val Ala Val Lys Ala Val Gly Glu Glu Thr Phe Arg  
 115               120                   125  
  
 Leu Cys Arg Glu Leu Val Asp Gly Ile Val Met Val Ser Arg Asp Ala  
 130               135                   140  
  
 Ile Cys Ala Ser Ile Lys Asp Met Phe Glu Glu Lys Arg Ser Ile Leu  
 145               150                   155                   160  
  
 Glu Pro Ala Gly Ala Leu Ala Leu Ala Gly Ala Glu Ala Tyr Cys Lys  
 165               170                   175  
  
 Tyr Tyr Asn Leu Lys Gly Glu Thr Val Val Ala Ile Thr Ser Gly Ala  
 180               185                   190  
  
 Asn Met Asn Phe Asp Arg Leu Arg Leu Val Thr Glu Leu Ala Asp Val  
 195               200                   205  
  
 Gly Arg Lys Arg Glu Ala Val Leu Ala Thr Phe Leu Pro Glu Arg Gln  
 210               215                   220

Gly Ser Phe Lys Lys Phe Thr Glu Leu Val Gly Arg Met Asn Ile Thr  
 225 230 235 240

Glu Phe Lys Tyr Arg Tyr Asp Ser Asn Ala Lys Asp Ala Leu Val Leu  
 245 250 255

Tyr Ser Val Gly Ile Tyr Thr Asp Asn Glu Leu Gly Ala Met Met Asp  
 260 265 270

Arg Met Glu Ser Ala Lys Leu Arg Thr Val Asn Leu Thr Asp Asn Asp  
 275 280 285

Leu Ala Lys Asp His Leu Arg Tyr Phe Ile Gly Gly Arg Ser Glu Ile  
 290 295 300

Lys Asp Glu Leu Val Tyr Arg Phe Ile Phe Pro Glu Arg Pro Gly Ala  
 305 310 315 320

Leu Met Lys Phe Leu Asp Thr Phe Ser Pro Arg Trp Asn Ile Ser Leu  
 325 330 335

Phe His Tyr Arg Ala Gln Gly Glu Ala Gly Ala Asn Val Leu Val Gly  
 340 345 350

Ile Gln Val Pro Pro Ala Glu Phe Asp Glu Phe Lys Ser His Ala Asn  
 355 360 365

Asn Leu Gly Tyr Glu Tyr Met Ser Glu His Asn Asn Glu Ile Tyr Arg  
 370 375 380

Leu Leu Leu Arg Asp Pro Lys Val  
 385 390

## (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 728 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: sf11.pk0055.h7

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAAATATTGT AGCAATAACC AGTGGAGCAA ACATGAATT TGATAAACCT CGGGTTGTAA	60
CTGAACTTGC TAATGTTGGT CGTAAACAAG AGGCTGTGCT GGCAACTGTT ATGGCAGAGG	120
AGCCTGGCAG TTTCAAACAA TTTTGTGAAT TGGTGGGGCA GATGAACATA ACAGAATTCA	180
AATACAGATA TAACTCAAAT GAGAAGGCAG TTGTCCTTTA CAGTGTGGG GTTCACACAA	240
TCTCCGAACT AAGAGCAATG CAGGAGAGGA TGGAATCTTC TCAGCTCAA ACTTACAATC	300
TCACAGAAAG TGACTTGGTG AAAGACCACT TGGCTTACTT GATGGGAGGC CGATCAAACG	360
TTCAGAATGA GGTCTTTGTC GTCTCACCTT TCCAAGAAAG ACTGGTGCTT TGATGAAATT	420
TTTGGACCCCT TCAGTCCACG TTGGGATATT AGTTTATCCA TTACCGAGGG GAGGTGAAAC	480
TGGAGCAAAC TGCTAGTTGG NTACAGGTAC CAAAATGAGA TAGATGAGTC CATGATCGTG	540

CTAACAAACT GGATATGATT ATAAGTGGNA ATATGTGATG NCTCAGCTCA ATCNCGATGG	600
GGNTTAAGCA CTGCATATGG GNATTAGGG NAGNTACANT TAAATTACAG GCCTCAAGNT	660
AAGCATANTN TAGGAACTAG CTTTACAGGG GGCTACNANT TAACCGNGTA TTTTTTTGA	720
GATGANNG	728

## (2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 152 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: sf11.pk0055.h7

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Asn Ile Val Ala Ile Thr Ser Gly Ala Asn Met Asn Phe Asp Lys Leu			
1	5	10	15
Arg Val Val Thr Glu Leu Ala Asn Val Gly Arg Lys Gln Glu Ala Val			
20	25	30	
Leu Ala Thr Val Met Ala Glu Glu Pro Gly Ser Phe Lys Gln Phe Cys			
35	40	45	
Glu Leu Val Gly Gln Met Asn Ile Thr Glu Phe Lys Tyr Arg Tyr Asn			
50	55	60	
Ser Asn Glu Lys Ala Val Val Leu Tyr Ser Val Gly Val His Thr Ile			
65	70	75	80
Ser Glu Leu Arg Ala Met Gln Glu Arg Met Glu Ser Ser Gln Leu Lys			
85	90	95	
Thr Tyr Asn Leu Thr Glu Ser Asp Leu Val Lys Asp His Leu Arg Tyr			
100	105	110	
Leu Met Gly Gly Arg Ser Asn Val Gln Asn Glu Val Phe Val Val Ser			
115	120	125	
Pro Xaa Pro Arg Lys Thr Gly Ala Leu Met Lys Phe Leu Asp Xaa Phe			
130	135	140	
Ser Pro Arg Trp Asp Ile Ser Leu			
145	150		

## (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 572 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: sre.pk0044.f3

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AAAGACCTGG TGCTTGATG AAATTTGG ACCCCTTCAG TCCACGTTGG AATATCAGTT	60
TATTCATTA CCGAGGGGAG GGTGAAACTG GAGCAAATGT GCTAGTTGGA ATACAGGTAC	120
CCAAAAGTGA GATGGATGAG TTCCACGATC GTGCCAACAA ACTTGGATAT GATTATAAAG	180
TGGTGAATAA TGATGATGAC TTCCAGCTTC TAATGCACTG ATGATGGTT TAGGCAC TTG	240
CCATTATTGT GTATTTAGT CAACAAGTTT GCCATATTAA ATATTCAC GGTGTTCT	300
AAAAGTTGGA TGGGGAAAAA AGGTGGAAAG GAAGTGGCCT TCAGACATGT CATTAGTTGA	360
TTAGAGGAAC AACTAGTTCT TTTTACCTAA TGCGGCGTCT TATTACATTT TTTATAATCT	420
GTAATTTATG TTTTTTGT GTTGTAAACA TTGGAATCTT ATAATGTTGT TGCCTGGTCT	480
TTTGTGTCTG TAATATAAGT GTCTCAAAA GGTGTTGC TAAATTCAG CAGCCTAAAA	540
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA	572

## (2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 72 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: sre.pk0044.f3

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Arg Pro Gly Ala Leu Met Lys Phe Leu Asp Pro Phe Ser Pro Arg Trp			
1	5	10	15

Asn Ile Ser Leu Phe His Tyr Arg Gly Glu Gly Glu Thr Gly Ala Asn		
20	25	30

Val Leu Val Gly Ile Gln Val Pro Lys Ser Glu Met Asp Glu Phe His		
35	40	45

Asp Arg Ala Asn Lys Leu Gly Tyr Asp Tyr Lys Val Val Asn Asn Asp		
50	55	60

Asp Asp Phe Gln Leu Leu Met His	
65	70

## (2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 507 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Burkholderia capacia

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ala Ser His Asp Tyr Leu Lys Lys Ile Leu Thr Ala Arg Val Tyr  
 1 5 10 15

Asp Val Ala Phe Glu Thr Glu Leu Glu Pro Ala Arg Asn Leu Ser Ala  
 20 25 30

Arg Leu Arg Asn Pro Val Tyr Leu Lys Arg Glu Asp Asn Gln Pro Val  
 35 40 45

Phe Ser Phe Lys Leu Arg Gly Ala Tyr Asn Lys Met Ala His Ile Pro  
 50 55 60

Ala Asp Ala Leu Ala Arg Gly Val Ile Thr Ala Ser Ala Gly Asn His  
 65 70 75 80

Ala Gln Gly Val Ala Phe Ser Ala Ala Arg Met Gly Val Lys Ala Val  
 85 90 95

Ile Val Val Pro Val Thr Thr Pro Gln Val Lys Val Asp Ala Val Arg  
 100 105 110

Ala His Gly Gly Pro Gly Val Glu Val Ile Gln Ala Gly Glu Ser Tyr  
 115 120 125

Ser Asp Ala Tyr Ala His Ala Leu Lys Val Gln Glu Glu Arg Gly Leu  
 130 135 140

Thr Phe Val His Pro Phe Asp Asp Pro Tyr Val Ile Ala Gly Gln Gly  
 145 150 155 160

Thr Ile Ala Met Glu Ile Leu Arg Gln His Gln Gly Pro Ile His Ala  
 165 170 175

Ile Phe Val Pro Ile Gly Gly Gly Leu Ala Ala Gly Val Ala Ala  
 180 185 190

Tyr Val Lys Ala Val Arg Pro Glu Ile Lys Val Ile Gly Val Gln Ala  
 195 200 205

Glu Asp Ser Cys Ala Met Ala Gln Ser Leu Gln Ala Gly Lys Arg Val  
 210 215 220

Glu Leu Ala Glu Val Gly Leu Phe Ala Asp Gly Thr Ala Val Lys Leu  
 225 230 235 240

Val Gly Glu Glu Thr Phe Arg Leu Cys Lys Glu Tyr Leu Asp Gly Val  
 245 250 255

Val Thr Val Asp Thr Asp Ala Leu Cys Ala Ala Ile Lys Asp Val Phe  
 260 265 270

Gln Asp Thr Arg Ser Val Leu Glu Pro Ser Gly Ala Leu Ala Val Ala  
 275 280 285

Gly Ala Lys Leu Tyr Ala Glu Arg Glu Gly Ile Glu Asn Gln Thr Leu  
 290 295 300

Val Ala Val Thr Ser Gly Ala Asn Met Asn Phe Asp Arg Met Arg Phe  
 305 310 315 320

Val Ala Glu Arg Ala Glu Val Gly Glu Ala Arg Glu Ala Val Phe Ala  
 325 330 335

Val Thr Ile Pro Glu Glu Arg Gly Ser Phe Lys Arg Phe Cys Ser Leu  
 340 345 350  
 Val Gly Asp Arg Asn Val Thr Glu Phe Asn Tyr Arg Ile Ala Asp Ala  
 355 360 365  
 Gln Ser Ala His Ile Phe Val Gly Val Gln Ile Arg Arg Arg Gly Glu  
 370 375 380  
 Ser Ala Asp Ile Ala Ala Asn Phe Glu Ser His Gly Phe Lys Thr Ala  
 385 390 395 400  
 Asp Leu Thr His Asp Glu Leu Ser Lys Glu His Ile Arg Tyr Met Val  
 405 410 415  
 Gly Gly Arg Ser Pro Leu Ala Leu Asp Glu Arg Leu Phe Arg Phe Glu  
 420 425 430  
 Phe Pro Glu Arg Pro Gly Ala Leu Met Lys Phe Leu Ser Ser Met Ala  
 435 440 445  
 Pro Asp Trp Asn Ile Ser Leu Phe His Tyr Arg Asn Gln Gly Ala Asp  
 450 455 460  
 Tyr Ser Ser Ile Leu Val Gly Leu Gln Val Pro Gln Ala Asp His Ala  
 465 470 475 480  
 Glu Phe Glu Arg Phe Leu Ala Ala Leu Gly Tyr Pro Tyr Val Glu Glu  
 485 490 495  
 Ser Ala Asn Pro Ala Tyr Arg Leu Phe Leu Ser  
 500 505

## (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1582 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: cc3.mn0002d2

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ACGAGACGAG TCCCCCTCCCC CCACCTCGCC TCACCCAACC GGAAACGAACA AGTTACCATC	60
TCATCCCAAC CCCGCCTCGA CGGGATCTCG TCGGACTCGG ATCCGCCCGA CCACCCCGCG	120
CCGCCCGAGA TCAAAGAAGA TGGCAGCTCT CGACACCTTC CTCTTCACCT CGGAGTCTGT	180
GAACGAGGGA CACCCCTGACA AGCTCTGCGA CCAGGTCTCA GATGCCGTTTC TTGACGCTTG	240
CCTTGCTGAG GACCCTGACA GCAAGGTTGC TTGTGAGACC TGCACCAAGA CCAACATGGT	300
CATGGTCTTT GGTGAGATCA CCACCAAGGC CAATGTCGAC TACGAGAAGA TTGTCAGGGGA	360
GACCTGCCGC AACATTGGTT TTGTGTCAAA CGATGTCGGG CTTGACGCTG ACCACTGCAA	420
GGTGCTCGTG AACATTGAGC AGCAGTCCCC TGATATTGCT CAGGGTGTGC ATGGCCACTT	480
CACCAAGCGC CCCGAGGAGA TTGGAGCTGG TGACCAGGGGA CACATGTTCG GGTATGCGAC	540

CGATGAGACC CCTGAGTTGA TGCCCCTCAG CCATGTCCTT GCCACCAAGC TAGGTGCTCG	600
TCTCACCGAG GTCCGCAAGA ACGGAACCTG CCCCTGGCTC AGCCCTGATG GGAAGACCCA	660
GGTGACAGTC GAGTACCGCA ATGAGGGTGG TGCCATGGTC CCCATCCGTG TCCACACCGT	720
CCTCATCTCC ACCCAGCACG ACGAGACAGT GACCAATGAT GAGATCGCTG CTGACCTGAA	780
GGAGCATGTC ATCAAGCCTA TCATCCCTGA GCAGTACCTT GACGAGAAGA CCATCTTCCA	840
CCTTAACCCA TCCGGCCGCT TTGTCATTGG TGGACCTCAC GGCGATGCTG GCCTCACTGG	900
CCGCAAGATC ATCATTGACA CCTACGGTGG CTGGGGAGCC CATGGCGGTG GCGCTTCTC	960
CGGCAAGGAC CCAACCAAGG TTGACCGCAG CGGAGCCTAT GTCGCGAGGC AGGCTGCCAA	1020
GAGCATCGTC GCCAGCGGCC TTGCTCGCCG CGCCATCGTC CAGGTGTCTT ACGCCATCGG	1080
CGTGCCCCGAG CCTCTCTCCG TGTTTGTGCA CACGTACGGC ACCGGCGCGA TCCCCGACAA	1140
GGAGATCCTC AAGATTGTCA AGGAGAACTT CGATTCAGG CCTGGCATGA TTATCATCAA	1200
CCTTGACCTC AAGAAAGGCC GCAACGGCG CTACCTCAAG ACGGCAGCCT ACGGCCACTT	1260
CGGAAGGGAC GACCTGACT TCACCTGGGA GGTGGTGAAG CCACTCAAGT CGGAGAAACC	1320
TTCTGCCCTAA GGCGGCCTTT TTTTCAGTAA GAAGCTTTG GTGGTCTGCT GTGCTTAATC	1380
ATGCTTTAT ATGGCTTCTA CATGTTGTGG TTCTTCTTG ATCTGCACCG CGCTTATCGT	1440
TTGTGTTGTA CTGCCCTAAT AAGTGGTGCT TATGAGGACT GTTTCTGGTT TTGCTGCTTA	1500
TGTTGTAATG CTTGAAACA ATGAAAGAACG CTACAGGCCA CAGCTATTT GAGAAGTAAT	1560
GGAACCTCGT GCCGTTTGA TT	1582

## (2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 396 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: cc3.mn0002.d2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Ala Ala Leu Asp Thr Phe Leu Phe Thr Ser Glu Ser Val Asn Glu			
1	5	10	15

Gly His Pro Asp Lys Leu Cys Asp Gln Val Ser Asp Ala Val Leu Asp			
20	25	30	

Ala Cys Leu Ala Glu Asp Pro Asp Ser Lys Val Ala Cys Glu Thr Cys			
35	40	45	

Thr Lys Thr Asn Met Val Met Val Phe Gly Glu Ile Thr Thr Lys Ala			
50	55	60	

Asn Val Asp Tyr Glu Lys Ile Val Arg Glu Thr Cys Arg Asn Ile Gly			
65	70	75	80

Phe Val Ser Asn Asp Val Gly Leu Asp Ala Asp His Cys Lys Val Leu  
 85 90 95

Val Asn Ile Glu Gln Gln Ser Pro Asp Ile Ala Gln Gly Val His Gly  
 100 105 110

His Phe Thr Lys Arg Pro Glu Glu Ile Gly Ala Gly Asp Gln Gly His  
 115 120 125

Met Phe Gly Tyr Ala Thr Asp Glu Thr Pro Glu Leu Met Pro Leu Ser  
 130 135 140

His Val Leu Ala Thr Lys Leu Gly Ala Arg Leu Thr Glu Val Arg Lys  
 145 150 155 160

Asn Gly Thr Cys Pro Trp Leu Arg Pro Asp Gly Lys Thr Gln Val Thr  
 165 170 175

Val Glu Tyr Arg Asn Glu Gly Gly Ala Met Val Pro Ile Arg Val His  
 180 185 190

Thr Val Leu Ile Ser Thr Gln His Asp Glu Thr Val Thr Asn Asp Glu  
 195 200 205

Ile Ala Ala Asp Leu Lys Glu His Val Ile Lys Pro Ile Ile Pro Glu  
 210 215 220

Gln Tyr Leu Asp Glu Lys Thr Ile Phe His Leu Asn Pro Ser Gly Arg  
 225 230 235 240

Phe Val Ile Gly Gly Pro His Gly Asp Ala Gly Leu Thr Gly Arg Lys  
 245 250 255

Ile Ile Ile Asp Thr Tyr Gly Gly Trp Gly Ala His Gly Gly Ala  
 260 265 270

Phe Ser Gly Lys Asp Pro Thr Lys Val Asp Arg Ser Gly Ala Tyr Val  
 275 280 285

Ala Arg Gln Ala Ala Lys Ser Ile Val Ala Ser Gly Leu Ala Arg Arg  
 290 295 300

Ala Ile Val Gln Val Ser Tyr Ala Ile Gly Val Pro Glu Pro Leu Ser  
 305 310 315 320

Val Phe Val Asp Thr Tyr Gly Thr Gly Ala Ile Pro Asp Lys Glu Ile  
 325 330 335

Leu Lys Ile Val Lys Glu Asn Phe Asp Phe Arg Pro Gly Met Ile Ile  
 340 345 350

Ile Asn Leu Asp Leu Lys Lys Gly Gly Asn Gly Arg Tyr Leu Lys Thr  
 355 360 365

Ala Ala Tyr Gly His Phe Gly Arg Asp Asp Pro Asp Phe Thr Trp Glu  
 370 375 380

Val Val Lys Pro Leu Lys Ser Glu Lys Pro Ser Ala  
 385 390 395

## (2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2183 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Oryza sativa

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAATTCTTAT AAATGAACGG AAAATGGAAA AAAAAATTGA TTGGTGCCAC TTCAAAGTTA	60
AATATGCCAA GACGAATTGA TATGTTCTG CTGTTGTTT ATGCTCTTGA TTAGTTGATG	120
CGCATGTTCA ATGATTATG ATGTTTGCT TTGTGGAAAG ATTACATGTA AAGAGTATAG	180
TAGAACCCCT AAAAGCTAGC CAGCGATTTC GCTCTTTTT TCCAGGTCTC CATGATATGT	240
TTACCCCTAA AAGTGGTATA TTTATGTGAT AGTTACAATA CATACTGGAC CACGATTGAT	300
TATGCGTTA TGCTGATTCC GGCAGAAAAT TGTAGATTTC CTTGTGCTCT ATACCTGCTT	360
GTTGCGCTTG TAGAGAATAT TACAAATACC TAACACTTGC CCAAGGAAC TAGGAACCTA	420
GTCAACTCTT TGTAGGGACA ACTATTAG CCCAAAATTG TGGTCTTGTG AGGTGCCAAC	480
AAAACAGCAT CTTGGCGTAC ATAAGCTATA TAGAGGATTA AAAGGAATGT TTTGTTCCCT	540
GCTACTGTTT TTTAACCTG TTTACTCAGG ACAAAATTG TTGCATAAAC CATTGTTCT	600
AGGGATCAGT ATTGTCCTCT CAGTGTGTTA TGTAAGCATT TCCAGAAATC AATTGTCGCT	660
ATCAGCTTCC CTCACATTAG CTATCACCTA TACCCCTTT TTTCTCATAG GCTCACCATG	720
TCCATTTAT TCATGATATT TCTTTGCTA AAGTATGTGA AATACCATT TATGCAGATA	780
GGAGAAGATG GCCGCACTTG ATACCTCCT CTTTACCTCG GAGTCTGTGA ACGAGGGCCA	840
CCCTGACAAG CTCTGCGACC AAGTCTCAGA TGCTGTGCTT GATGCCTGCC TCGCCGAGGA	900
CCCTGACAGC AAGGTCGCTT GTGAGACCTG CACCAAGACA AACATGGTCA TGGTCTTGG	960
TGAGATCACC ACCAAGGCTA ACGTTGACTA TGAGAAGATT GTCAGGGAGA CATGCCGTAA	1020
CATCGGTTTT GTGTCAGCTG ATGTCGGTCT CGATGCTGAC CACTGCAAGG TGCTTGTGAA	1080
CATCGAGCAG CAGTCCCCTG ACATTGCACA GGGTGTGCAC GGGCACTTCA CCAAGCGCCC	1140
TGAGGAGATT GGTGCTGGTG ACCAGGGACA CATGTTGGA TATGCAACTG ATGAGACCCC	1200
TGAGTTGATG CCCCTCAGCC ATGTCCTTGC TACCAAGCTT GGCCTCGTC TTACGGAGGT	1260
TCGCAAGAAT GGGACCTGCG CATGGCTCAG GCCTGACGGG AAGACCCAAG TGACTGTTGA	1320
GTACCGCAAT GAGAGCGGTG CCAGGGTCCC TGTCCTGTC CACACCGTCC TCATCTCTAC	1380
CCAGCGATGAT GAGACAGTCA CCAACGATGA GATTGCTGCT GACCTGAAGG AGCATGTCAT	1440
CAAGCCTGTC ATTCCCAGGC AGTACCTTGA TGAGAAGACA ATCTTCCATC TTAACCCATC	1500
TGGTCGCTTC GTCATTGGCG GACCTCATGG TGATGCTGGT CTCACTGCC GGAAGATCAT	1560
CATTGACACT TATGGTGGCT GGGGAGCTCA CGGTGGTGGT GCCTTCTCTG GCAAGGACCC	1620
AACCAAGGTT GACCGCAGTG GAGCATACTG CGCAAGGCAA GCTGCCAAGA GCATTGTTGC	1680

TAGTGGCCTT GCTCGCCGCT GCATTGTCCA AGTATCATAc GCCATCGGTG TCCCAGAGCC	1740
ACTGTCCGTA TTCGTCGACA CATA CGGCAC TGGCAGGATC CCTGACAAGG AGATCCTCAA	1800
GATTGTGAAG GAGAACTTCG ACTTCAGGCC TGGCATGATC ATCATCAACC TTGACCTCAA	1860
GAAAGGCGGC AACGGACGCT ACCTCAAGAC GGCGGTTAC GGTCACTTCG GAAGGGACGA	1920
CCCAGACTTC ACCTGGGAGG TGGTGAAGCC CCTCAAGTGG GAGAAGCCTT CTGCCTAAAA	1980
GCTCCCTTTC GGAGGTTTT GCTCTGTCCC ATTATGGTGT TTTGTTTCCT CGCTGCTCAG	2040
CATTGTGATT CTTAACCTGC CCCCGCTGC CATTATGCC CATGCACGCT ACTTTCTAA	2100
TAATAAGTAC TTATAAGGGT ATTGTGTTG AATATTTAC CTAGAGGAGG AGGAGGATTT	2160
GTTATCTGTT ATTGCTTAAG CTT	2183

## (2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1485 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: s2.12b06

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGCCAAGCCC CACTCAACCA CCACACCACT CTCTCTGCTC TTCTTCTACC TTTCAAGTTT	60
TTAAAGTATT AAGATGGCAG AGACATTCT ATTACCTCA GAGTCAGTGA ACGAGGGACA	120
CCCTGACAAG CTCTGCGACC AAATCTCCGA TGCTGTCCTC GACGCTTGCC TTGAACAGGA	180
CCCAGACAGC AAGGTTGCCT GCGAAACATG CACCAAGACC AACTTGGTCA TGGTCTTCGG	240
AGAGATCACC ACCAAGGCCA ACAGTTGACTA CGAGAAAGATC GTGCGTGACA CCTGCAGGAA	300
CATCGGCTTC GTCTCAAACG ATGTGGACT TGATGCTGAC AACTGCAAGG TCCTTGTAAA	360
CATTGAGCAG CAGAGCCCTG ATATTGCCA GGGTGTGCAC GGCCACCTTA CCAAAAGACC	420
CGAGGAAATC GGTGCTGGAG ACCAGGGTCA CATGTTGGC TATGCCACGG ACGAAACCCC	480
AGAATTGATG CCATTGAGTC ATGTTCTTGC AACTAAACTC GGTGCTCGTC TCACCGAGGT	540
TCGCAAGAAC GGAACCTGCC CATGGTTGAG GCCTGATGGG AAAACCCAAG TGACTGTTGA	600
GTATTACAAT GACAACGGTG CCATGGTTCC AGTCGTGTC CACACTGTGC TTATCTCCAC	660
CCAACATGAT GAGACTGTGA CCAACGACGA AATTGCAAGT GACCTCAAGG AGCATGTGAT	720
CAAGCCGGTG ATCCCCGAGA AGTACCTTGA TGAGAAGACC ATTTTCCACT TGAAACCCCTC	780
TGGCCGTTT GTCATTGGAG GTCTCTCACGG TGATGCTGGT CTCACCGGCC GCAAGATCAT	840
CATCGATACT TACGGAGGAT GGGGTGCTCA TGGTGGTGGT GCTTTCTCCG GGAAGGATCC	900
CACCAAGGTT GATAGGAGTG GTGCTTACAT TGTGAGACAG GCTGCTAAGA GCATTGTGGC	960
AAGTGGACTA GCCAGAAGGT GCATTGTGCA AGTGTCTTAT GCCATTGGTG TGCCCGAGCC	1020

TTTGTCTGTC	TTTGTGACA	CCTATGGCAC	CGGGAAGATC	CATGATAAGG	AGATTCTCAA	1080
CATTGTGAAG	GAGAACTTG	ATTCAGGCC	CGGTATGATC	TCCATCAACC	TTGATCTCAA	1140
GAGGGGTGGG	AATAACAGGT	TCTTGAAGAC	TGCTGCATAT	GGACACTTCG	GCAGAGAGGA	1200
CCCTGACTTC	ACATGGGAAG	TGGTCAAGCC	CCTCAAGTGG	GAGAAGGCCT	AAGGCCATTC	1260
ATTCCACTGC	AATGTGCTGG	GAGTTTTTA	GC GTTGC CCT	TATAATGTCT	ATTATCCATA	1320
ACTTTCCACG	TCCCTTGCTC	TGTGTTTTC	TCTCGTCGTC	CTCCTCCTAT	TTGTTTCTC	1380
CTGCCTTCA	TTTGTAAATT	TTTACATGAT	CAACTAAAAA	ATGTACTCTC	TGTTTCCGA	1440
CCATTGTGTC	TCTTAATATC	AGTATCAAAA	AGAATGTTCC	AAGTT		1485

## (2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 392 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: s2.12b06

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Ala Glu Thr Phe Leu Phe Thr Ser Glu Ser Val Asn Glu Gly His  
 1                   5                   10                   15

Pro Asp Lys Leu Cys Asp Gln Ile Ser Asp Ala Val Leu Asp Ala Cys  
 20                 25                 30

Leu Glu Gln Asp Pro Asp Ser Lys Val Ala Cys Glu Thr Cys Thr Lys  
 35                 40                 45

Thr Asn Leu Val Met Val Phe Gly Glu Ile Thr Thr Lys Ala Asn Val  
 50                 55                 60

Asp Tyr Glu Lys Ile Val Arg Asp Thr Cys Arg Asn Ile Gly Phe Val  
 65                 70                 75                 80

Ser Asn Asp Val Gly Leu Asp Ala Asp Asn Cys Lys Val Leu Val Asn  
 85                 90                 95

Ile Glu Gln Gln Ser Pro Asp Ile Ala Gln Gly Val His Gly His Leu  
 100               105                 110

Thr Lys Arg Pro Glu Glu Ile Gly Ala Gly Asp Gln Gly His Met Phe  
 115               120                 125

Gly Tyr Ala Thr Asp Glu Thr Pro Glu Leu Met Pro Leu Ser His Val  
 130               135                 140

Leu Ala Thr Lys Leu Gly Ala Arg Leu Thr Glu Val Arg Lys Asn Gly  
 145               150                 155                 160

Thr Cys Pro Trp Leu Arg Pro Asp Gly Lys Thr Gln Val Thr Val Glu  
 165               170                 175

Tyr Tyr Asn Asp Asn Gly Ala Met Val Pro Val Arg Val His Thr Val  
 180 185 190

Leu Ile Ser Thr Gln His Asp Glu Thr Val Thr Asn Asp Glu Ile Ala  
 195 200 205

Ala Asp Leu Lys Glu His Val Ile Lys Pro Val Ile Pro Glu Lys Tyr  
 210 215 220

Leu Asp Glu Lys Thr Ile Phe His Leu Asn Pro Ser Gly Arg Phe Val  
 225 230 235 240

Ile Gly Gly Pro His Gly Asp Ala Gly Leu Thr Gly Arg Lys Ile Ile  
 245 250 255

Ile Asp Thr Tyr Gly Gly Trp Gly Ala His Gly Gly Ala Phe Ser  
 260 265 270

Gly Lys Asp Pro Thr Lys Val Asp Arg Ser Gly Ala Tyr Ile Val Arg  
 275 280 285

Gln Ala Ala Lys Ser Ile Val Ala Ser Gly Leu Ala Arg Arg Cys Ile  
 290 295 300

Val Gln Val Ser Tyr Ala Ile Gly Val Pro Glu Pro Leu Ser Val Phe  
 305 310 315 320

Val Asp Thr Tyr Gly Thr Gly Lys Ile His Asp Lys Glu Ile Leu Asn  
 325 330 335

Ile Val Lys Glu Asn Phe Asp Phe Arg Pro Gly Met Ile Ser Ile Asn  
 340 345 350

Leu Asp Leu Lys Arg Gly Gly Asn Asn Arg Phe Leu Lys Thr Ala Ala  
 355 360 365

Tyr Gly His Phe Gly Arg Glu Asp Pro Asp Phe Thr Trp Glu Val Val  
 370 375 380

Lys Pro Leu Lys Trp Glu Lys Ala  
 385 390

## (2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1479 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Lycopersicon esculentum*

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAATTCCCTAC AAAGAGGTTA TTTCTCTCAA GGGGTAAAAAA GATTGCCCTT TTTCGACATT	60
TATAATCCTC TTTTTCTCTT TGTTCGCCGT TGGGTTCTTC ACTTTCTGT TTCTTGAGAA	120
TGGAAACTTT CTTATTCACC TCCGAGTCTG TGAACGAGGG TCACCCAGAC AAGCTCTGTG	180
ATCAGATCTC TGATGCAGTT CTTGATGCCT GCCTTGAGCA AGATCCCGAG AGCAAAGTTG	240
CATGTGAAAC TTGCACCAAG ACCAACTTGG TCATGGTCTT TGGTGAGATC ACAACCAAGG	300

CTATTGTAGA CTATGAGAAG ATTGTGCGTG ACACATGCCG TAATATTGGA TTTGTTCTG	360
ATGATGTTGG TCTTGATGCT GACAACGTCA AGGTCTTGT TTACATTGAG CAGCAAAGTC	420
CTGATATTGC TCAAGGTGTC CACGGCCATC TGACCAAACG CCCCGAGGAG ATTGGTGCTG	480
GTGACCAGGG CCACATGTT GGCTATGCAA CAGATGAGAC CCCTGAATTA ATGCCTCTCA	540
GTCACGTGCT TCCAACCTAAA CTTGGTGCCC GTCTTACAGA AGTCCGCAAG AATGGCACCT	600
GCGCCTGGTT GAGGCCTGAT GGCAAGACCC AAGTTACTGT TGAGTATAGC AATGACAATG	660
GTGCCATGGT TCCAATTAGG GTACACACTG TTCTTATCTC CACCCAACAC GATGAGACCG	720
TTACCAATGA TGAGATTGCC CGCGACCTTA AGGAGCATGT CATCAAACCA GTCATCCCAG	780
AGAAAGTACCT TGATGAGAAT ACTATTTCC ACCTTAACCC ATCTGGCCGA TTCGTTATTG	840
GTGGACCTCA TGGTGATGCT GGTCTCACTG GTCGTAAAAT CATCATCGAC ACTTATGGTG	900
CTTGGGGTGC TCATGGTGGT GGTGCTTCT CGGGCAAAGA CCCAACCAAG GTCGACAGGA	960
GTGGTGCATA CATTGTAAGG CAGGCTGCAA AGAGTATCGT AGCTAGTGGA CTTGCTCGTA	1020
GATGCATCGT GCAGGTATCT TATGCCATCG GTGTGCCTGA GCCATTGTCT GTATTGTTG	1080
ACACCTATGG CACTGGAAAG ATCCCTGACA GGGAAATTTT GAAGATCGTT AAGGAGAACT	1140
TTGACTTCAG ACCTGGAATG ATGTCCATTA ACTTGGATTG GAAGAGGGGT GGCAATAGAA	1200
GATTCTTGAA AACTGCTGCC TATGGTCACT TTGGACGTGA TGACCCGAT TTCACATGGG	1260
AAGTTGTCAA GCCCCTCAAG TGGGAAAAGC CCCAAGACTA ATAAGTGCTT GCCTATGTTT	1320
TTGTTCTTG TTGTTTGCTT GTGGCTTAG AATCTCCCCC GTGTTGCTT GTTTGCTTT	1380
GTATTTCTC TTTTGACCTT TTATTTGTT ATTGTCTGT TTCCATTGTG TTGGATGGAT	1440
ATCTTAGGCC TTGGAATATT AAGGAAAGAA AAGGAATTC	1479

## (2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCTCCCTTC GGTTCATCGG CCTCCCGATC GAGCAGTAGA AGCAGCGCAA GGGCATCGCT	60
AGCACTAAAG AAATGGCAGC CGAGACGTTG CTCTTCACGT CCGAGTCTGT GAACGGAGGGC	120
CATCCCGACA AGCTCTGTGA CCAAGTCTCC GACGCCGTCT TGGATGCCTG CTTGGCCAG	180
GATGCCGACA GCAAGGTGCG CTGCGAGACC GTCACCAAGA CCAACATGGT CATGGCTTG	240
GGCGAGATCA CCACCAAGGC CACCGTCGAC TATGAGAAGA TCGTGCCTGA CACCTGCCGC	300
AACATCGGTT TCATCTCTGA TGACGTTGGT CTCGACGCCG ACCGTTGCAA RGTGCTCGTC	360
AACATCGAGC AGCAGTCCCC TGACATTGCC CAGGGTGTTC ATGGACACTT CACCAAGCGT	420

CCCGAAGAAC	TGGCGCCGG	TGACCAGGGC	ATCATGTTG	GCTATGCCAC	CGATGAGACC	480
CCTGAGCTGA	TGCCCCCAA	GCACGTGCTT	GCCACCAAGC	TYGGAGCTCG	CCTCACSGAG	540
GTCCGCAAGA	ATGGCACCTG	CGCCTGGTC	AGGCCTGACG	GAAAGACCCA	GGTCACAGTC	600
GAGTACCTAA	ACGAGGATGG	TGCCATGGTA	'CCTGTTCGTG	TGCACACCCT	CCTCATCTCC	660
ACCCAGCACG	ACGAGACCGT	CACCAACGAC	GAGATTGCTG	CGGACCTCAA	GGAGCATGTC	720
ATCAAGCCGG	TGATCCCCGC	AAAGTACCTC	GATGAGAACAA	CCATCTTCCA	CCTGAACCCG	780
TCTGGCCGCT	TCGTCATCGG	CGGCCCCAC	GGTGACGCCG	GTCTCACCGG	CCGCAAGATC	840
ATCATCGACA	CCTATGGTGG	CTGGGGAGCC	CACGGCGGCCG	GTGCCTTCTC	TGGCAAGGAC	900
CCAACCAAGG	TCGACCGYAG	TGGCGCCTAC	ATTGCCAGGC	ARGCCGCCAA	GAGCATCATC	960
GCCAGCGGCC	TCGCACGCCG	CTGCATTGTG	CAGATCTCAT	ACGCCATCGG	TGTGCCTGAG	1020
CCTTTGTCTG	TGTTCGTCGA	CTCCTACGGC	ACCGGCAAGA	TCCCCGACAG	GGAGATCCTC	1080
AAGCTCGTGA	AGGAGAACTT	TGACTTCAGG	CCCAGGATGA	TCAGCATCAA	CCTGGACTTG	1140
AAGAAAAGGTG	GAAACAGGTT	CATCAAGACC	GCTGCTTACG	GTCACTTTGG	CCGTGATGAT	1200
GCCGACTTCA	CCTGGGAGGT	GGTGAAGCCC	CTCAAGTTCG	ACAAGGCATC	TGCCTAAGAG	1260
CATGGCATTTC	TCTTGGTCTG	CCGCCTCTCA	AGTCGTCAA	GACGGGATCA	TGTTGCTCCT	1320
GGGAAGTGGG	AAGAACATT	AGACATTGAA	GCGACGCTCT	ACACTGGTCT	TGTTGTATGG	1380

## (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 394 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Ala	Ala	Glu	Thr	Phe	Leu	Phe	Thr	Ser	Glu	Ser	Val	Asn	Glu	Gly
1						5			10			15			
His	Pro	Asp	Lys	Leu	Cys	Asp	Gln	Val	Ser	Asp	Ala	Val	Leu	Asp	Ala
						20		25			30				
Cys	Leu	Ala	Gln	Asp	Ala	Asp	Ser	Lys	Val	Ala	Cys	Glu	Thr	Val	Thr
						35		40			45				
Lys	Thr	Asn	Met	Val	Met	Val	Leu	Gly	Glu	Ile	Thr	Thr	Lys	Ala	Thr
						50		55			60				
Val	Asp	Tyr	Glu	Lys	Ile	Val	Arg	Asp	Thr	Cys	Arg	Asn	Ile	Gly	Phe
						65		70		75		80			
Ile	Ser	Asp	Asp	Val	Gly	Leu	Asp	Ala	Asp	Arg	Cys	Lys	Val	Leu	Val
						85		90			95				
Asn	Ile	Glu	Gln	Gln	Ser	Pro	Asp	Ile	Ala	Gln	Gly	Val	His	Gly	His
						100		105			110				

Phe Thr Lys Arg Pro Glu Glu Val Gly Ala Gly Asp Gln Gly Ile Met  
 115 120 125  
 Phe Gly Tyr Ala Thr Asp Glu Thr Pro Glu Leu Met Pro Leu Lys His  
 130 135 140  
 Val Leu Ala Thr Lys Leu Gly Ala Arg Leu Thr Glu Val Arg Lys Asn  
 145 150 155 160  
 Gly Thr Cys Ala Trp Val Arg Pro Asp Gly Lys Thr Gln Val Thr Val  
 165 170 175  
 Glu Tyr Leu Asn Glu Asp Gly Ala Met Val Pro Val Arg Val His Thr  
 180 185 190  
 Val Leu Ile Ser Thr Gln His Asp Glu Thr Val Thr Asn Asp Glu Ile  
 195 200 205  
 Ala Ala Asp Leu Lys Glu His Val Ile Lys Pro Val Ile Pro Ala Lys  
 210 215 220  
 Tyr Leu Asp Glu Asn Thr Ile Phe His Leu Asn Pro Ser Gly Arg Phe  
 225 230 235 240  
 Val Ile Gly Gly Pro His Gly Asp Ala Gly Leu Thr Gly Arg Lys Ile  
 245 250 255  
 Ile Ile Asp Thr Tyr Gly Trp Gly Ala His Gly Gly Ala Phe  
 260 265 270  
 Ser Gly Lys Asp Pro Thr Lys Val Asp Arg Ser Gly Ala Tyr Ile Ala  
 275 280 285  
 Arg Gln Ala Ala Lys Ser Ile Ile Ala Ser Gly Leu Ala Arg Arg Cys  
 290 295 300  
 Ile Val Gln Ile Ser Tyr Ala Ile Gly Val Pro Glu Pro Leu Ser Val  
 305 310 315 320  
 Phe Val Asp Ser Tyr Gly Thr Gly Lys Ile Pro Asp Arg Glu Ile Leu  
 325 330 335  
 Lys Leu Val Lys Glu Asn Phe Asp Phe Arg Pro Gly Met Ile Ser Ile  
 340 345 350  
 Asn Leu Asp Leu Lys Lys Gly Asn Arg Phe Ile Lys Thr Ala Ala  
 355 360 365  
 Tyr Gly His Phe Gly Arg Asp Asp Ala Asp Phe Thr Trp Glu Val Val  
 370 375 380  
 Lys Pro Leu Lys Phe Asp Lys Ala Ser Ala  
 385 390

## (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1353 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Hordeum vulgare

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAATTCCGGA TAGCATCAGC ACAACTGCAC GAGAGCATCT CTACCACCAA AGAAATGGCG	60
GCCGAGACGT TCCTCTTCAC GTCCGAGTCC GTGAACGAGG GCCATCCCGA CAAGCTGTGC	120
GACCAGGTCT CTGACGCCGT CTTGGACGCC TGCTTGGCCC AGGATCCTGA CAGCAAGGTT	180
GCTTGCAGA CCTGCACCAA GACCAACATG GTCACTGGTCT TCGGCGAGAT CACCACCAAG	240
GCCACCGTTG ACTATGAGAA GATTGTGCGC GACACCTGCC GTGACATCGG CTTCATCTCT	300
GACGACGTCG GTCTCGATGC CGACCATTGC AAGGTGCTCG TCAACATCGA GCAGCAATCC	360
CCTGACATTG CCCAGGGTGT TCACGGACAC TTCACCAAGC GTCCAGAAGA GGTCGGCGCC	420
GGTGACCAAGG GCATCATGTT TGGCTACGCC ACTGATGAGA CCCCTGAGCT GATGCCCTC	480
ACCCACATGC TTGCCACCAA GCTCGGAGCT CGCCTCACCG AGGTCCGCAA GAATGGCACC	540
TGCGCCTGGC TCAGGCCTGA TGGAAAGACC CAGGTCACCA TTGAGTACCT AAACGAGGGT	600
GGTGCCATGG TGCCCCTTCG TGTGCACACC GTCCTCATCT CCACCCAGCA TGATGAGACC	660
GTCACCAACG ATGAGATCGC TGCAGACCTC AAGGAGCATG TCATCAAGCC GGTGATTCCC	720
GGGAAGTACC TCGATGAGAA CACCATCTTC CACCTGAACC CATCGGGCCG CTTTGTCAATC	780
GGTGGCCCTC ACGGCGATGC CGGTCTCACC GCCCGCAAGA TCATCATCGA CACCTATGGT	840
GGCTGGGAG CCCACGGCGG CGGTGCCCTC TCTGGCAAGG ACCCTACCAA GGTCGACCGC	900
AGTGGCGCCT ACATTGCCAG GCAGGCTGCC AAGAGCATCA TCGCCAGCGG CCTCGCACGC	960
CGGTGCATTG TGCAGATCTC ATATGCCATC GGTGTACCTG AGCCTTGTC TGTGTTGTC	1020
GAECTCTACG GCACTGGCAA GATCCCTGAC AGGGAGATCC TCAAGCTCGT GAAGGAGAAC	1080
TTTGACTTCA GACCCGGGAT GATCACCGATC AACCTCGACT TGAAGAAAGG TGGAAACAGG	1140
TTCATCAAGA CAGCTGCTTA CGGTCACCTT GGCGCGATG ATGCTGACTT CACCTGGGAG	1200
GTGGTGAAGC CCCTCAAGTT CGACAAGGCA TCTGCTTAAG AAGAAGACAT CACATTGAGG	1260
GTTCTTCTTG GTCTGATGCC TCTCAAGTTC GGCAAGGCGG GATCCTTTG CTCCCTGGAA	1320
GTAAGAAGAA GCATTCAACA TCGCCCCGAA TTC	1353